

/translation>"MASTIKEALSWEDQSLFECAYGSPHLAKTEMATSSSEYQQT
SKWSPRVPOODWT-SOPBARVTIKMECNPNQNCNSPNSBDDCSVAKCKMYSSENDDWGM

RESULT	HUMERG2	3166 bp ss-RNA	PRI	08-NOV-1994
LOCUS	Human erg2 gene	encoding erg2 protein, complete cds.		
DEFINITION				
ACCESSION	MT1254			
NID	9182186			
KEYWORDS	erg 2 protein.			
SOURCE	Human cell line COLO 320, cDNA to mRNA, clone lambda 12.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3166)			
AUTHORS	Rao, V.N., Papas, T.S. and Reddy, E.S.			
TITLE	e.g., a human ets-related gene on chromosome 21: alternative splicing, polyadenylation, and translation			
JOURNAL	Science 237 (4815), 635-639 (1987)			
MEDLINE	87263429			
FEATURES	Location/Qualifiers			
SOURCE	1 3166			

LOCUS	9	S45205	1673 bp	mRNA	PRT	05-JAN-1993
DEFINITION	F11-1-Friend leukemia integration 1 [human, mRNA, 1673 nt].					
ACCESSION	S42025					
NID	9257353					
KEYWORDS	.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1673)					
AUTHORS	Prasad,D.D., Rao,V.N. and Reddy,E.S.					
TITLE	Structure and expression of human F11-1 gene					
JOURNAL	Cancer Res. 52 (20), 5833-5837 (1992)					
MEDLINE	93007976					
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbb 115336] from the original journal article. This sequence comes from Fig. 1A.					
FEATURES	Location/Qualifiers					
OWNER	1673					

Search completed: sat Apr 10 10:21:10 1999
Job time : 3786 secs.

Db	241	TQRITRPPDLPVQEARRSAWTSHTSHSHPTQKATQPSSTVVKTEQDFQFOLPQILGPTT	300
OY	241	TORITRPPDLPVQEARRSAWTSHTSHSHPTQKATQPSSTVVKTEQDFQFOLPQILGPTT	300
Db	301	RUANPSSGQIQLWQFLLELLSPSSNSNCITTWEGTNGERKMTDPEVARWGERKSCKPNM	360
OY	301	RUANPSSGQIQLWQFLLELLSPSSNSNCITTWEGTNGERKMTDPEVARWGERKSCKPNM	360
Db	361	YDKLSRALRYYDKNMTKHKRYAKFDFHIGIAQALQPHPESSMYKP-SDLPMSS	419
OY	361	YDKLSRALRYYDKNMTKHKRYAKFDFHIGIAQALQPHPESSMYKP-SDLPMSS	419
Db	420	YHAHPQMNFWAHPHPALPVTSSSFFAARNPYWNNSPTGGIYPTNRLPAAHMPHLGTYY	478
OY	420	PHAHQPMNFVAHPHPALPVTSSSFFAARNPYWNNSPTGGIYPTNRLPAAHMPHLGTYY	478
RESULT	2		
ID	014319	PRELIMINARY; PRT; 385 AA.	
	014319;		
	01-NOV-1996 (TREMBLREL. 01, CREATED)		
	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	FLI-1.		
GN	HOMO SAPIENS (HUMAN).		
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	BUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
TISSUE=BLOOD;			
RX	MEDLINE: 93176799.		
RA	HROMAS R., MAY W., DENNY C., RASKIND W., MOORE J., MAKI R.A., BECK E.,		
RA	KLEMAS M.J.; BIOCHEM. BIOPHYS. ACTA 1172:155-158(1993).		
RL	EMBL: M93255; G182661; -.		
DR	PROSITE; PS00345; ETS DOMAIN_1; 1.		
DR	PROSITE; PS00346; ETS_DOMAIN_2; 1.		
DR	PFAM; PF00178; Ets.		
DR	SEQUENCE 385 AA; 43437 MW; 0820C243 CRC32;		
Query Match	Best Local Similarity 46.4%; Score 1401; DB 4; Length 385; Matches 229; Conservative 69; Mismatches 73; Indels 35; Gaps 21; Score 1401; DB 4; Length 385; Matches 229; Conservative 69; Mismatches 73; Indels 35; Gaps 21;		
Db	10	ARESPVPCSVSKSLVGGGESNPVNNSYMBEKNGPPPNNMTNERVIVPADLVHQ 69	
OY	78	SRNSPDCCSVAKGKMKVSSDNVGMNNGSYMEKH-IPPPNNMTNERRIVPADLWST 136	
Db	70	EHVRQWLEWAKEYSLMEDIISFFQNMDGKECLKMKNKEDFLRATLYTEVILSHLSYR 129	
OY	137	DHVROWLEWAVKEYEGLDILFONIDKELGKMTDQEQTSPSNADILSHLHLTR 196	
Db	130	ESSL--LAYNTTSHT-DOSSRL-SVKE--D---P--S-Y-DSV-R--R-G-AWGNM 168	
OY	197	ETPLPHLTSDDVAKLONSPRLHARNITGGATIFPNNTSVYBATORITRPPDLPYEQR 256	
Db	169	NSG-LNNS-PPLG-GAQ---TISKNEQRPOPDPYQIGPSSRLANGPSQIQLMFL 221	
OY	257	RSAWTSHSHPTOSKATOPSSSTVPKTEDQRPQLDPYQIGPSSRLANGPSQIQLMFL 316	
Db	222	LELSDSANASCITWEGTNGERKMTDDEVARWQORKSKPNMNDKLSSRALRYYDKNI 281	
OY	317	LELSSOSSNSNCITWEGTNGERKMTDDEVARWQORKSKPNMNDKLSSRALRYYDKNI 376	
Db	282	MTKVHGKRYAKFDFHIGIAQALQPHPTESMSMRYP-SDISYMPSYHAKQKYNVPHRS 340	
OY	377	MTKVHGKRYAKFDFHIGIAQALQPHPTESMSMRYP-SDISYMPSYHAKQKYNVPHRS 340	
Db	341	SMVPTSSFGASQYKTS-TGIGIYPNPVPHPNTHVPSHLGSYV 385	
OY	436	ALPVTTSSFFAARNPYWNNSPTGGIYPTNRLPAAHMPHLGTYY 478	
RESULT	3		
ID	016199	PRELIMINARY; PRT; 254 AA.	
AC	016199;		
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1996 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	EWS-ERG FUSION PROTEIN TYPE 1E (FRAGMENT).		
GN	EWS ERG.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
RA	EUDANTONI M., BIESEL J.A., SERRA M., WANG J.Y., WEI Y.H., NYCUM L.,		
RA	EMANUEL B.S., EVANS G.A.,		
RL	J. CLIN. INVEST. 94:489-496(1994).		
DR	EMBL; S72855; G633778; -.		
DR	PROSITE; PS00345; ETS DOMAIN_1; 1.		
DR	PROSITE; PS00346; ETS_DOMAIN_2; 1.		
FT	NON_TER 00178 1 Ets.		
SQ	SEQUENCE 254 AA; 2857 MW; 596580CD CRC32;		
Query Match	Score 36.5%; DB 4; Length 254; Best Local Similarity 77.7%; Pred. No. 5.03e-250; Mismatches 20; Indels 3; Gaps 3;		
Matches	178; Conservative 20; Mismatches 20;		
Db	27	QONIYPYEPRRSAWTSHSHPT-QSKATQPSSTVVKTEQDFQFOLPQDLYQTLGPNSSSRLANP 86	
OY	247	RPDIFYEQARRSAWTSHSHPT-QSKATQPSSTVVKTEQDFQFOLPQDLYQTLGPNSSSRLANP 305	
Db	87	GSGQIQLWQFLLELLSDSSNSNCITTWEGTNGERKMTDPEVARWGERKSCKPNMNYDKLS 146	
OY	306	GSGQIQLWQFLLELLSDSSNSNCITTWEGTNGERKMTDPEVARWGERKSCKPNMNYDKLS 365	
Db	147	RALRYYDKNIMTKHKRYAKFDFHIGIAQALQPHPTESMSMRYP-SDLPYNSYHGRYAKFDFHIGIAQALQPHRS 254	
OY	366	RALRYYDKNIMTKHKRYAKFDFHIGIAQALQPHPTESMSMRYP-SDLPYNSYHGRYAKFDFHIGIAQALQPHRS 424	
Db	206	OKMNIVAPHPALPVTSSSFFAARNPYWNNSPTGGIYPTNRLPAAHMPHS 254	
OY	425	OKMNIVAPHPALPVTSSSFFAARNPYWNNSPTGGIYPTNRLPAAHMPHS 478	
RESULT	4		
ID	016203	PRELIMINARY; PRT; 196 AA.	
AC	016203;		
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1996 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	EWS-ERG-EWS-ERG FUSION PROTEIN TYPE 9E (FRAGMENT).		
GN	EWS-ERG.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	BUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
TISSUE=BLOOD;			
RX	MEDLINE: 94314948.		
RA	GOVANNINI M., BIESEL J.A., SERRA M., WANG J.Y., WEI Y.H., NYCUM L.,		
RA	EMANUEL B.S., EVANS G.A.,		
RL	J. CLIN. INVEST. 94:489-496(1994).		
DR	EMBL; S72855; G633778; -.		
DR	PROSITE; PS00345; ETS DOMAIN_1; 1.		
DR	PROSITE; PS00346; ETS_DOMAIN_2; 1.		
DR	PFAM; PF00178; Ets.		
FT	NON_TER 00178 1 Ets.		
SQ	SEQUENCE 196 AA; 22268 MW; FBCD632E CRC32;		
Query Match	Score 26.4%; DB 4; Length 196; Best Local Similarity 73.3%; Pred. No. 5.52e-170; Mismatches 20; Indels 20; Gaps 20;		

Db 22 SSSGQQSSQIQIOWQFLELLSSNSNCITWEGTNGEKFMDPDEVARWGERKSPN 81
 Qy || :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 C4DB.4.
 299 SSRILANGPGSGQIQLQFLELLSSNSNCITWEGTNGEKFMDPDEVARWGERKSEN 38
 OC CAENORHABDITIS ELEGANS.
 Db 82 MYNKLRSRALRYYDKNIMTKVHKRYAKFDFEGIAQALQPHPPESLYKYP-SLPLPM 140
 Qy ||||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
 359 MNYKLRSRALRYYDKNIMTKVHKPRESS-MYKPSDLPMSSYHGKRYAKFDFHGIQA 417
 Db 141 GSYVHPOKENFYVPHPPALPVTSSEAPNPWNPSGGIYNTLTHMSH 196
 Qy 418 LQPRAHPQKINFVPHPPALPVTSSEAPNPWNPSGGIYNTLRAHMHS 473
 OS CAENORHABDITIS ELEGANS.
 OC EUARIOTA; METIZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 RESULT 5 PRELIMINARY; PRT; 188 AA.
 ID Q2355; 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 AC 02255; 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DT DT COSMID T08H4.
 T08H4. 3.
 OS CAENORHABDITIS ELEGANS.
 OC EUARYOTA; METIZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=BRISTOL N2;
 RC MEDLINE; 94150718.
 RX BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
 DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
 HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
 KIRSEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 McMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
 RIFFEN L., ROOPRA A., SAUNDERS D., SHONKEEN R., SMALDON N., SMITH A.,
 SONNHAMMER E., STADEN R., SUSTON J., THIERRY-MIEG J., THOMAS K.,
 VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
 WILKINSON-SPROUT J., WOLDMAN P.;
 NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RN HALSWORTH K.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX WATERSTON R.;
 DR SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
 EMBL; U5966; G1293845; -.
 PROSITE; PS0045; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00345; ETS_DOMAIN_2; 1.
 DR PEAM; PF00178; Ets.
 SQ SEQUENCE 208 AA; 22664 MW; 3492097D CRC32;
 Query Match 16.0%; Score 555; DB 5; Length 208;
 Best Local Similarity 72.6%; Pred. No. 5.77e 90;
 Matches 69; Conservative 14; Mismatches 11; Indels 1; Gaps 1;
 RA STELLYES L.;
 RA SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RL EMBL; U39470; G1041871; -.
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PFAM; PF00178; Ets.
 DR PFAM; PF00178; Ets_DOMAIN_2; 1.
 RA SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA WATERSTON R.;
 RA SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RL EMBL; U39470; G1041871; -.
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PFAM; PF00178; Ets.
 DR PFAM; PF00178; Ets_DOMAIN_2; 1.
 RA SEQUENCE 188 AA; 21345 MW; C98FD1EC CRC32;
 RESULT 7 PRELIMINARY; PRT; 238 AA.
 ID 099531; 01-MAY-1997 (TREMBLREL. 03, CREATED)
 AC 099531; 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DT DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DE FEV PROTEIN.
 OS HOMO SAPIENS (HUMAN).
 OC EUARYOTA; METIZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PETER, COUROT J., PACOUEMENT H., MICHON J., THOMAS G.,
 RA MAGDELÉNAT H., DELAUTURE O.;
 RL ONCOENE 14:1159-1164 (1997).
 DR EMBL; Y08976; B291921; -.
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 DR PFAM; PF00178; Ets.
 SQ SEQUENCE 238 AA; 25030 MW; D4057DD0 CRC32;
 Query Match 15.7%; Score 543; DB 4; Length 238;
 Best Local Similarity 73.7%; Pred. No. 2.35e 87; Indels 2; Gaps 2;

RN [1] SEQUENCE FROM N.A.
 RP TPSYNADILSLHLHYLERGATEFIPNTSYPEATORITRPLDPEQAHRSAWTHSHP : |
 RC STRAIN=BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA BURTON J., CONNELL M., COSEY T., COOPER J., COULSON A., CRAXTON M.,
 RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
 RA HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
 RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
 RA RIFKEN L., ROOPRA A., SAUNDERS D., SHOWMANNEEN R., SMALDON N., SMITH A.,
 RA SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPROAT J., WOHLDAWAN P.;
 RL NATURE 368:32-38(1994).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=BRISTOL N2;
 RA HALLSWORTH K.;
 RA SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDJB DATA BANKS.
 RN [3] SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DDJB DATA BANKS.
 DR EMBL; U56986; GL293845; .
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 DR PFAM; PF00178; Ets;
 SO SEQUENCE 208 AA; 22664 MW; 3492097D CRC32;
 Query Match 20.2%; Score 664; DB 5; Length 208;
 Best Local Similarity 79.4%; Pred. No. 1.84e-122; Mismatches 81; Indels 0; Gaps 0;
 Matches 14; Mismatches 7; Indels 0; Gaps 0;
 Db 21 GPMMAILSATCQGQLWOFLELLADAVNATCIAEBSNGEKKFLVPDEARKWGRKS 80
 Qy 269 GPTSSRLANPGSGQIQLWOFLELLSDSSNSNCITWEGTNGEFKMTDPDEARRWGRKS 328
 Db 81 KPMNMYDKLSRALRYYDKNMTKVQKRYAKFDFEHGIAA 370
 Qy 329 KPMNMYDKLSRALRYYDKNMTKVQKRYAKFDFEHGIAA 370
 RESULT 9 ID 091744 PRELIMINARY; PRT; 268 AA.
 ID 062804 PRELIMINARY; PRT; 336 AA.
 AC 062804; DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 AC 062804; DT 01-NOV-1995 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 AC 062804; DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 FT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE TRANSCRIPTION FACTOR GABP ALPHA SUBUNIT (FRAGMENT).
 OS OTIS ARIES (SHEEP).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1] SEQUENCE FROM N.A.
 RP EZASHI T., EALY A.D., OSTROWSKI M.C., ROBERTS R.M.;
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DDJB DATA BANKS.
 EMBL; AF057717; G3046690; -.
 DR PROSITE; PS00345; ETS DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS DOMAIN_2; 1.
 FT NON_TER 1
 SO SEQUENCE 336 AA; 38033 MW; 8CFEE91F CRC32;
 Query Match 19.8%; Score 650; DB 6; Length 336;
 Best Local Similarity 41.6%; Pred. No. 3.78e-119; Mismatches 101; Indels 51; Gaps 20; Gaps 15;
 Matches 61; Mismatches 61; Indels 20; Gaps 15;
 Db 58 EQERLGIPDYDQWSQDQVHLHWVWNKEFSMDIDLTTL-NISGRELCSLSQEDPFRV 116
 Qy 121 NERRVIVPADPLWLSIDHVROMLWAVKEVGLPDVVLQNIDSKEICKMKTFDDF-ORL 179
 Db 117 -PR- GEIWMHSLER-K--VWLASQE- QMMNE-IVTI-DQP-WQIIPAS-VOSATP 163
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA EZASHI T., EALY A.D., OSTROWSKI M.C., ROBERTS R.M.;
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DDJB DATA BANKS.
 EMBL; AF057716; G3046689; -.
 DR PROSITE; PS00345; ETS DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS DOMAIN_2; 1.

QY 180 TPSYNADILSLHLHYLERGATEFIPNTSYPEATORITRPLDPEQAHRSAWTHSHP : |
 Db 164 TAIKAIN-SIKAQVQ-RAPRISGEDRSR-GNRITGN-NGQIQIWFQFIELLTDKAR 218
 QY 240 TQSQAQPSSSTVPKTEDQRQLDPQIQLSPQTSSRLANPQSGQIQLWQFELLSDSNS 299
 Db 219 DCISWYGDEGERFKLNQPELVAKWQWSORKRNKPTMNYEKLSLALRYYDGDMICKYQKREV 278
 QY 300 NCITWEGTNGEFKMTDPDEARRWGRKSXPNNYDKLSRALRYYDKNMTKVHGKYA 359
 QY 360 YKF 281
 QY 360 YKF 362

DT 01-JUN-1998 (TREMBREL, 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL, 07, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN TRANSCRIPTION FACTOR PEA3.
GN PEA3.
OS BRACHYDANTO RERIO (ZEBRAFISH) (ZEBRA DANTO).
OC EUKARYOTA; METAZOA; CHORDAT; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA BROWN L.A., AMORES A., SCHILLING T.F., JOWETT T., BAERT J.L.,
RA DE LAUNOT Y., SHARROCKS A.D.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ003200; E1234815; -.
DR PROSITE; PS00345; ETS_DOMAIN; 1.
DR PROSITE; PS00346; ETS_DOMAIN; 2; 1.
SQ SEQUENCE 494 AA; 55620 MW; 249CBBC CRC32;

Query Match 13.4%; Score 440; DB 13; Length 494;
Best Local Similarity 62.2%; Pred. No. 2.76e70; Indels 0;
Matches 51; Conservative 13; Mismatches 18; Gaps 0;

Db 348 GSLOQWQFLVALLDPSNAHFIANTGRGMFKLIEPEEVARLWGSIEKNRPAWNNDKLRS 407
Qy |:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 281 QGQDQWQFLLELLDSDSSNSNCITMEGTNGEKKMDPDEVARRWWRKSRKSPNMDNDKLRA 340

Db 408 LRYYKEKGIMQKVAGERYVVF 429
Qy |||||:||| ||| ||| |||:|||:
Qy 341 LRYYDKNIMTKVHGKRYAYKF 362

Search completed: Wed Apr 7 09:36:38 1999
Job time : 122 secs.

		BASE COUNT	191 a	272 c	162 g	137 t
Db	949 CCCTCCGTTACTACTATGACAGAACATCAGCACCAAGGTCCATTGGAGGCCATCCCT 1008	ORIGIN				
Qy	1162 caactcgctactactatgacaaatatattatgactaaagtccatggtaacgcgttatgc 1221	Query Match	29.2%	Score 446;	DB 26;	Length 762;
Db	1009 ACGATTCGACTTCACGGATGCCAGGCCCTCACCCCCACCCGGAGTCATCTC 1068	Best Local Similarity	80.0%	Pred. No. 0.00e+00;	Mismatches 0;	
Qy	1222 acbaatttgatttccacggaaatcgcttggccctccggcttccacccccaatccagaatccca 1281	Matches	569;	Conservative	Indels 3;	Gaps 1;
Db	1069 TGTACAAGTACCCCTCAGACCTCCGATCGGCCTATACGCCCACAGAGA 1128	Db	86 ATTACCATATGAGCCCCAGGAGATCAGCCCTGGACCGGTCACGGCACCCACGGCCC 145			
Qy	1282 tgcataaataccatcaagacctccatcatgaggatccataccatgcacaccccaagaga 1341	Qy	808 atttacattatgacaaggcggagatcagggtggacgagacacggcatccact--- 864			
Db	1129 TGTACTTGTCGGCCGACCCAGCCGGTACGGTTCAGTTTGCTG 1188	Db	146 AGTCGAAAGCTCAACCATCCTTCACAGTGCCAAACTGAGAACGACAGGTCTC 205			
Qy	1342 tgaatttgtatgttcacccctcgatgttgcgcgttaacctatccatccatcgtttgtctg 1401	Qy	865 agtcaaaagtcaccaaccaatcttcacatcgatgtggccaaacacagaaacgcacgcgcctc 924			
Db	1189 CCCAACCCATACTGGAAITCACCAACTGGGTATATACCCACACTAGGCTCCC 1248	Db	206 AGTAGATCCTATACATTCTGGACCAACAGTAAGTGGCTGCAAATCAGGAGTG 265			
Qy	1402 cccttaatccatacttggaaatccaccaactggggatctacccaaataccaggctgccg 1461	Qy	925 atttagtgcctatccatcgatgttgcacactactaa 1499			
Db	1249 CCAGCCATATGCCCTCATCTGGCACTTACACTAA 1286	Db	326 GCATCACCTGGAGGACCCACGGGAGTCAAGTGAAGTACGATCCGGACAGGAGTGGCC 385			
Qy	1462 ctgcataatgcctccatctgtgcacactactaa	Qy	1045 gcatcacctggaggagcaaaatggggatctcaagatgcacagacccctgatggatgtggctc 1104			
RESULT	5	LOCUS	S72621	762 bp mRNA	PRI	24-JAN-1995
DEFINITION	EWS . .erg (translocation, type 1e and 9el) [human, SK-PN-LI cell]	ORGANISM	Homo sapiens			
ACCESSION	S72621	REFERENCE	1	(bases 1 to 762)	AUTHORS	Giovannini,M., Biegel,J.A., Serra,M., Wang,J.Y., Wei,Y.H., Nycum,L., Emmanuel,B.S. and Evans,G.A.
NID	9633773	TITLE			JOURNAL	primitive neuroectodermal tumors with variant translocations J.Clin. Invest. 94 (2), 489-496 (1994)
KEYWORDS	REMARK	MEDLINE	94314948	REMARK	REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 153609] from the original journal article. This sequence comes from Fig. 2A.. Map location: t(21;22)(q22;q12).
SOURCE	FEATURES	source		Location/Qualifiers		
gene						
		RESULT	6	LOCUS	AP000022	133746 bp DNA
		DEFINITION		HOME sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 15'15, complete sequence.	PRI	13-MAY-1998
CDS		ACCESSION	AP000022	NID	93132332	
		KEYWORDS		ORGANISM	Homo sapiens	
		SOURCE		PRIMATES; Cetacean; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
		ORGANISM		REFERENCE	1 (bases 1 to 133746)	
				AUTHORS	Hirakawa,M., Yamaguchi,H. and Imai,K.	
				TITLE	Homo sapiens 1,296,826bp genomic DNA of 21q22.2 Down Syndrome region	
gene				JOURNAL	Published Only in DataBase (1998) In Press	
				REFERENCE	2 (bases 1 to 133746)	

RESULT	8
LOCUS	CCRNALFL 3490 bp mRNA
DEFINITION	Coturnix coturnix mRNA for transcription factor FLI, clone 10.1.
ACCESSION	V14773
NID	9326302
KEYWORDS	fl1 gene; FLI oncoprotein; transcription factor.
SOURCE	ORGANISM Coturnix coturnix. Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
REFERENCE	1 (bases 1 to 3490)
AUTHORS	Mager,A.M., Grapin-Botton,A., Ladjali,K., Meyer,D., Wolff,C.M., Stieglar,P., Bonnin,M.A. and Remy,P.
JOURNAL	The avian fl1 gene is specifically expressed during embryogenesis in a subset of neural crest cells giving rise to mesenchyme Int. J. Dev. Biol. 42 (4), 561-572 (1998)
MEDLINE	9835803
REVIEWER	2 (bases 1 to 3490)
AUTHORS	Stieglar,P.
TITLE	Direct Submission
JOURNAL	Submitted (09-SEP-1997) P. Stieglar, Centre National de la Recherche Scientifique, U.P.R. 9005 du C.N.R.S, 15 Rue Rene Descartes, 67084 Strasbourg Cedex, FRANCE
COMMENT	Related sequence Y14774.
FEATURES	Location/Qualifiers
source	1. .3490 <organism="Coturnix coturnix" <db_xref="taxon:9091" <chromosome="1" <dev_stage="4-day quail embryo" <clone lib="pcDNA1" <clone="10.1" <map="q31-33" <map="q31-33" 215. .1513 215. .1513 <gene="fl1" <function="transcription factor" <codon_start=1 <product="FLI transcription factor" <ab_xref="PID:el308265" <db_xref="PID:93269303" <translation="MOTIVLVSISDQSLEFDSTGAAATHLPKADMATASGNPDYGO PHKINPUPPOQWINGQVRVNRKVNREVMHNSRESPDCSVNCKSKVAGIESNSPQ YSTMDERKGPPNMNTNERRVYPADEPTWQHEPWLEIAKEGLMEIDTTFQO NMDGEKCMNKDKFLRTSLYNTTEQSPQDPYQIIGPSSRLANGSGQDQMLNPFLELSRSRDN ASCTIWEGTNGESEFKMDPDEVARWRGERKSIRPNMTNDKLRLARYYDVKNTMKVKGK RYAKDFDFFGIGRQLQHPTESMKRPSKPSIMSPHSAHQVNFPVPHSSMPVIS SSFFGASSPYWTPSPASVYHNPVNPVRPHNAPHRVPHLGYY"
BASE COUNT	1026 a 770 c 752 g 942 t
ORIGIN	
Query Match	20.9%; score 320; DB 21; Length 3490;
Best Local Similarity	79.2%; Pred. No. 4.49e+263; Pairs 0; Mismatches 114; Indels 0; Gaps 0;
Matches	434; Conservative
db	910 AACAGAAGAGCAACGGGCCAACAGATCCATCAATTCTGGGCCACCAAGTAGTCG 969 905 acagagacccggcgcttcagttagatccatcgttgcacatctttggacccggccg 964
Qy	
db	970 TCTTGCCATACTGGAGTGGCAGATACACTGTGCAGTCTCCCTCGAGTTCTC 1029 tcttgcaaatccaggaggatggcagatacagactatggcagttctactggagttcttc 1024
Qy	
db	1030 GGACAGITCAAATGCCACGGTTCACATGGAGGGCACATGGGAATTCAAGAC 1089 ggacagactccaaacctccaaacttgcatacctggggggccaaatggggatcagagac 1084
Qy	
db	1025 ggacagactccaaacctccaaacttgcatacctggggggccaaatggggatcagagac 1084 AGACCCAGATGAAGTGGCAACGGGCCACAGATCCATCAATTCTGGGCCACCAAGTC 1029 tcttgcaaatccaggaggatggcagatacagactatggcagttctactggagttcttc 1024
Qy	
db	965 acagagacccggcgcttcagttagatccatcgttgcacatctttggacccggccg 964
Qy	
db	1030 GGACAGITCAAATGCCACGGTTCACATGGAGGGCACATGGGAATTCAAGAC 1089 ggacagactccaaacctccaaacttgcatacctggggggccaaatggggatcagagac 1084
Qy	
db	1025 ggacagactccaaacctccaaacttgcatacctggggggccaaatggggatcagagac 1084 AGACCCAGATGAAGTGGCAACGGGCCACAGATCCATCAATTCTGGGCCACCAAGTC 1029 tcttgcaaatccaggaggatggcagatacagactatggcagttctactggagttcttc 1024
Qy	
db	1085 acacccgtatggatggatggcggtttggggagagagagaaaaacccatcacatgtaca 1144
Qy	
RESULT	9
LOCUS	CCFLIONCO 3545 bp mRNA
DEFINITION	Coturnix coturnix mRNA for transcription factor FLI, clone 6.1.
ACCESSION	V14774
NID	93269304
KEYWORDS	fl1 gene; FLI oncoprotein; transcription factor.
SOURCE	ORGANISM Coturnix coturnix. Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
REFERENCE	1 (bases 1 to 3545)
AUTHORS	Mager,A.M., Grapin-Botton,A., Ladjali,K., Meyer,D., Wolff,C.M., Stieglar,P., Bonnin,M.A. and Remy,P.
JOURNAL	The avian fl1 gene is specifically expressed during embryogenesis in a subset of neural crest cells giving rise to mesenchyme Int. J. Dev. Biol. 42 (4), 561-572 (1998)
MEDLINE	9835803
REVIEWER	2 (bases 1 to 3545)
AUTHORS	Stieglar,P.
TITLE	Direct Submission
JOURNAL	Submitted (09-SEP-1997) P. Stieglar, Centre National de la Recherche Scientifique, U.P.R. 9005 du C.N.R.S, 15 Rue Rene Descartes, 67084 Strasbourg Cedex, FRANCE
COMMENT	Related sequence Y14773.
FEATURES	Location/Qualifiers
source	1. .3545 <organism="Coturnix coturnix" <db_xref="taxon:9091" <chromosome="1" <dev_stage="4-day quail embryo" <clone lib="pcDNA1" <clone="6.1" <map="q31-33" 396. .1595 <gene="fl1" <gene="fl1" 396. .1595 <gene="fl1" <function="transcription factor" <codon_start=1 <product="FLI transcription factor" <ab_xref="PID:el308263" <db_xref="PID:93269305" <translation="MTAGSNPQYQPKINPLPQQMINQPVNNKREVDHMGSR ESPVDCSINCKCSRLLVGACTESTENMSYSYMDKNGPPFMNTNERRVYPADEPTLWTQ ENVROWLEWAHYGLMEIDTTFQNDKGEKMKNDFLRTSLNTSEVILSHLY LRESSLIAVNPSPHSRTEASRSLATVQKPYACTONVNTKTEQRQDPYQIPLTSS RJANGSGQDQIQWQFLLELSDDSNASGTCWETNGERKMTDDEVARWRGERKSKPN

Search completed: Sat Apr 10 12:38:54 1999
Job time : 2833 secs.

320-398

#domain	ets	DNA-binding domain homology	#label ETS
#length	486	#molecular-weight	54608
#checksum	9577		

SUMMARY

Query Match 87.5%; Score 3032; DB 1; Length 486;
Best Local Similarity 87.5%; Pred. No. 0; 0 0e+00;
Matches 419; Conservative 28; Mismatches 29; Indels 3; Gaps 3;

Db 181 PSYNAIDLSSILHYLRETPHLHTSDDVVKALQNSPRLMHARNTGATFPNTSYPEA 240
Oy 181 PSYNADILLSLHLHYLRETPPLPHLTSDDVVKALQNSPRLMHARNTGATFPNTSYPEA 240

Db 241 TORITRDPDLYEQRSSAWNSHSHTQSATOPSSSTVPTEDQRQLPQYQIGPTSS 300
Oy 241 TORITRDPDLYEQRSSAWNSHSHTQSATOPSSSTVPTEDQRQLPQYQIGPTSS 300

Db 301 RLANPSGGQQLWQFQELLELSDSSNSNCITWEGTNGEFKMDPDEVARRGCKERSKPNM 360
Oy 301 RLANPSGGQQLWQFQELLELSDSSNSNCITWEGTNGEFKMDPDEVARRGCKERSKPNM 360

Db 361 YDKLSRALRYYDKNIMTKVHPPES-MYKPSDLPMSSYHGKRYAKEDFHGIAQALQ 419
Oy 361 YDKLSRALRYYDKNIMTKVHPPES-MYKPSDLPMSSYHGKRYAKEDFHGIAQALQ 419

Db 420 YHAPQKMNFVAPHPALPVISSFFAAPPNPYWNSPPTGGIYPNTRLPAAHMPSHLGTY 478
Oy 420 PHAPQKMNFVAPHPALPVISSFFAAPPNPYWNSPPTGGIYPNTRLPAAHMPSHLGTY 478

RESULT 2

ENTRY TVRIUEG #type complete
TITLE transforming protein erg-3 - human
CONTAINS transforming protein erg-1; transforming protein erg-2
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Mar-1989 #sequence_revision 30-May-1997 #text_change
ACCESSIONS A94294; A94178; A28041; A29515
REFERENCE #authors Rao, V.N.; Papas, T.S.; Shyam, E.; Reddy, P.
Science (1987) 237:635-639
#title erg, a human ets-related gene on chromosome 21: alternative splicing, polyadenylation, and translation.
#cross-references MUID:87263429
#accession A94294
##molecule_type mRNA
##cross-references 1-231, 256-486 #label REB
#cross-references GB:MI:7254; NID:9182186; PID:9182187

REFERENCE A94178

#authors Reddy, E.S.P.; Rao, V.N.;
Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6131-6135
#title The erg gene: a human gene related to the ets oncogene.
#accession A94178
##molecule_type mRNA
##cross-references MUID:87317608

REFERENCE 100-231, 256-486 ##label REB

#authors Prasad, D.D.; Rao, V.N.; Lee, L.; Reddy, E.S.
Oncogene (1994) 9:669-673
#title Differentially spliced erg-3 product functions as a transcriptional activator.

#cross-references MUID:94119611

#accession 158410
##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 230-259 ##label RES

GENETICS

#cross-references GDB:ERG
##cross-references GDB:119884; OMIM:165080
##map_position 21q22.2-21q22.2

CLASSIFICATION #superfamily: transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology

KEYWORDS alternative splicing; DNA binding; nucleus; proto-oncogene; transcription factor; transforming protein

FEATURE 1-231, 256-486 #product transforming protein erg-2 #status predicted
#label EG2\\
100-231, 256-486 #product transforming protein erg-1 #status predicted
#label EG1\\
126-200 #domain ets RII regulatory region homology #label ETS2\\

RESULT 3

ENTRY 137565 #type complete
TITLE transforming protein fil, long splice form - human Friend leukemia integration protein 1; transcription factor ERGB
CONTAINS #formal_name Homo sapiens #common_name man
ORGANISM #cross-references GB:M21535; NID:9182182; PID:9182185
#residues 100-231, 256-486 ##label REB
#cross-references MUID:87317608

REFERENCE 158410
Prasad, D.D.; Rao, V.N.; Lee, L.; Reddy, E.S.
Oncogene (1994) 9:669-673
#title Differentially spliced erg-3 product functions as a transcriptional activator.

#cross-references MUID:94119611

#accession 158410
##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 230-259 ##label RES

REFERENCE 137565
#cross-references MUID:92396239
#accession 137565
##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-452 ##label RES

REFERENCE S28843
#authors Hromas, R.; May, W.; Denny, C.; Raskind, W.; Moore, J.; Maki, R.A.; Beck, E.; Klemz, M.J.
#journal Biochim. Biophys. Acta (1993) 1172:155-158
#title Human F11-1 localizes to chromosome 11Q24 and has an aberrant transcript in neuroepithelioma.

#cross-references MUID:93116799
#accession S28843
##molecule_type mRNA
##residues 1-68, 'V', 70-129, 'A', 131-132, 'V', 134-322, 'Q', 324-425,
427-452 ##label HRO1

QY 1 MASTIREALSVVSEDOQLFECAYGSP-HLAKTEMPTASSSEYYGQTSKMSPRVPOQDWLSQ 59
Db 61 P-VRIVNKVREYD-HMNGRSRESPDCSVSKCNKLIGGGEANPMNNSYADEKNGPPPNM 117
| | :
QY 60 PPARYTIVKMECNPNOVNGSRSNPDCSVAKGGKVSSDNVNGYSGYMEKH-I-PPPNM 118
Db 118 TNERRVIVPADPAWSONHVRQLEWAKEYGLR-PDVILFQNIDGKECKMMDFLR 177
| | :
QY 119 TNERRVIVPADPLWSTDHVRQLEWAKEYGLR-PDVILFQNIDGKECKMMDFQR 178
Db 178 ATSAVTEVLISHYLRESSL-LAYNTSHT-DOSSRL-NVKE--D---P--S-Y- 222
| :
QY 179 LTPSI-NADILSHLHYRETLPLPHLTSDDVKALQNSPRLMHARNTGATFIFNTSVIP 230
Db 223 DSV-R--R-G-AWNNNMMSG-LINKS-PLIG-GSQ---TMGKNTEQRQOPDPQILGPT 269
| :
QY 239 EATORITTRPDLPYBQARRSAWTSHSHTPOSQATQPSSTVPKTEDORPQDLPQIOLGPT 298
Db 270 SRLANGPSQIQIQLQMFELLSNSDSSNSNCITWEGTNGEKFMDPDEVARWRGERSKPN 329
299 SRLANGPSQIQIQLQMFELLSNSDSSNSNCITWEGTNGEKFMDPDEVARWRGERSKPN 359
Db 330 MNYDKLRSRALRYYDKNIMKVKHRYAYKFDFFGIAQAOQPHPTSMKYP-SDISM 388
| :
QY 359 MNYDKLRSRALRYYDKNIMKVKHRYAYKFDFFGIAQAOQPHPTSMKYP-SDISM 417
Db 389 PSYHAHQKQNKVFVSHPSSMPVTSFFGASQWTSPTAGIYRPSVPRHPNTHVPSHL 449
| :
QY 418 LQPHAHQPKNFVAPHPALPVTSSESSFAAPNPWNPSPIGIVPN-T--RLPAAHMPSHL 474
Db 449 GSYV 452
| : :
QY 475 GTYY 478

RESULT 5
ENTRY
TITLE 549013 #type complete
ALTERNATE_NAMES Friend leukemia integration protein 1; transcription factor
ORGANISM ERGB
#formal_name Xenopus laevis #common_name African clawed frog
DATE 07-May-1995 #sequence_revision 23-May-1997 #text_change
05-Sep-1997
S49013
REFERENCE
#authors Meyer, D.; Wolff, C.M.; Stiegler, P.; Senan, F.; Befort, N.;
Mech. Dev. (1993) 44:109-121
#title Xf-fil, the Xenopus homologue of the fil-1 gene, is expressed during embryogenesis in a restricted pattern evocative of neural crest cell distribution.
#accession S49013
#status preliminary
##molecule_type mRNA
##residues 1-453 #label MEY
##cross-references EMBL:X66979; NID:9505486; PID:9505487

GENERICs
#gene f1
CLASSIFICATION #superfamily transcription factor erg; ets DNA-binding domain
#homology; ets RII regulatory region homology
KEYWORDS DNA binding; nucleus; proto-oncogene; transcription factor; transforming protein

FEATURE 117-191 #domain ets RII regulatory region homology #label ETS2\\
284-362 #domain ets DNA-binding domain homology #label ETS
SUMMARY #length 453 #molecular-weight 51015 #checksum 774

Query Match 50.2%; Score 1740; DB 1; Length 453;
Best Local Similarity 56.4%; Pred. No. 0.00e-00; Matches 273; Conservative 91; Mismatches 83; Indels 37; Gaps 25;

Db 1 MDGTEIKEALWSVSDOSLFSAYGASSHSLSKADWASANDYQGPHKINIPPOQDWING 60
| :
QY 1 MASTIREALSVVSEDOQLFECAYGSP-HLAKTEMPTASSSEYYGQTSKMSPRVPOQDWLSQ 59
Db 61 P-MRNKIKBEYE- HMNGRSRESPDCSINKSKLIGGEGNAMTY-TMDEKNGPPPNM 116
| | :
QY 60 PPARYTIVKMECNPNOVNGSRSNPDCSVAKGGKVSSDNVNGYSGYMEKH-I-PPPNM 118
Db 117 TNERRVIVPADPAWSONHVRQLEWAKEYGLR-PDVILFQNIDGKECKMMDFLR 176
| | :
QY 119 TNERRVIVPADPLWSTDHVRQLEWAKEYGLR-PDVILFQNIDGKECKMMDFQR 178
Db 177 STSINTEVILISHYLROSS-SSLYGYNQTAHT-DOSSRL-AKE--D---P--S-Y- 222
| :
QY 179 LTPSI-NADILSHLHYRETLPLPHLTSDDVKALQNSPRLMHARNTGATFIFNTSVIP 230
Db 223 EAV-R--RSGG-WGNSMSSP-VKSPPM-G-GTQ-NVNK-S-GDQQRSQPDQYQILGPT 270
| :
QY 239 EATORITTRPDLPYBQARRSAWTSHSHTPOSQATQPSSTVPKTEDORPQDLPQIOLGPT 298
Db 271 SRLANGPSQIQIQLQMFELLSNSDSSNSNCITWEGTNGEKFMDPDEVARWRGERSKPN 330
299 SRLANGPSQIQIQLQMFELLSNSDSSNSNCITWEGTNGEKFMDPDEVARWRGERSKPN 358
Db 331 MNYDKLRSRALRYYDKNIMKVKHRYAYKFDFFGIAQAOQPHPTSMKYP-SDISM 389
| :
QY 359 MNYDKLRSRALRYYDKNIMKVKHRYAYKFDFFGIAQAOQPHPTSMKYP-SDISM 417
Db 390 PSYHAHQKQNKVFVSHPSSMPVTSFFGASQWTSPTAGIYRPSVPRHPNTHVPSHL 449
| :
QY 418 LQPHAHQPKNFVAPHPALPVTSSESSFAAPNPWNPSPIGIVPN-T--RLPAAHMPSHL 474
Db 450 GGFY 453
| : :
QY 475 GTYY 478

RESULT 6
ENTRY A54617 #type fragment
TITLE transcription factor erg - mouse (fragment)
ALTERNATE_NAMES Ig heavy chain enhancer-binding protein
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
30-May-1997
ACCESSIONS A54617
REFERENCE A54617
#authors Rivera, R.R.; Stuiver, M.H.; Steenbergen, R.; Murro, C.
#Journal Mol. Cell. Biol. (1993) 13:1167-7169
#title Es proteins: new factors that regulate immunoglobulin heavy-chain gene expression.
#cross-references MUID:94019387
#accession A54617
#status preliminary
##molecule_type mRNA
##residues 1-272 #label RIV
#experimental_source pre-B-cell line 22D6
##note sequence extracted from NCBI backbone (NCBIN:138523,
NCBIP:138524)

CLASSIFICATION #superfamily transcription factor erg; ets DNA-binding domain
#homology; ets RII regulatory region homology
KEYWORDS DNA binding; phosphoprotein; proto-oncogene; transcription factor; transforming protein
FEATURE 140-218 #domain ets DNA-binding domain homology #label ETS
SUMMARY #length 272 #checksum 3754
Query Match 45.3%; Score 1571; DB 2; Length 272;
Best Local Similarity 82.4%; Pred. No. 6.02e-302; Matches 225; Conservative 17; Mismatches 28; Indels 3; Gaps 3;
Db 1 DDFQQLTPSVDNADILSHLHYRETLPLPHLTSDDVKALQNSPRLMHARNTGATFIPN 60
QY 174 DDFQQLTPSVDNADILSHLHYRETLPLPHLTSDDVKALQNSPRLMHARNTGATFIPN 233
Db 61 TSVPEATORITTRPDLPYBQARRSAWTSHSHTPOSQAAQSPSAVKTEDORPQDLPY 120

QY	234	TSVPEPTQRITRDPDIPYEARRSAMTSHSHT-QSKTQPSSTVPKTEDORQDPPY	292
Db	121	QIGLPTTSRRLANGPGSGQIQLWQPLLESDSSNSCITWEGTINGEKFMDPDEVARNGE	180
Db	293	QIGLPTTSRRLANGPGSGQIQLWQPLLESDSSNSCITWEGTINGEKFMDPDEVARNGE	352
Db	181	RKSKPNMYDKUSRALRYYDKNIMTKVHGKRYAKFDFHGINAQALQDPHPPESSLYKF-	239
QY	353	RKSKPNMYDKUSRALRYYDKNIMTKVHGKRYESS-MYKPSDLPYMSYHKGKRYAKFD	411
Db	240	SDLPYMSYHAPQMKMNVSPHPALPVTSSE	272
QY	412	HGIAQALQPHAPQMKMNFVAPHPPALPVTSSE	444
RESULT	7	S29844 # type complete	
ENTRY		transforming protein fli-1; short splice form - human	
TITLE		Friend leukemia integration protein 1; transcription factor	
ORGANISM		ERGB	
DATE		# formal_name Homo sapiens # common_name man	
ACCESSIONS		02-Dec-1993 #sequence_revision 23-May-1997 #text_change	
REFERENCE	S29844	02-Dec-1997	
#authors	S29843	R.A.; Beck, E.; Klemisz, M.J.	
#journal		Biochim. Biophys. Acta (1993) 1172:155-158	
#title		Human FLI-1 localizes to chromosome 11Q24 and has an aberrant transcript in neuroepithelioma.	
#cross-references	MURD:93176799		
#accession	S29844		
#status		preliminary: nucleic acid sequence not shown;	
#molecule_type		mRNA	
#note		#note	
GENETICS			
#gene		GDB:FLII	
#cross-references	GDB:127565; OMIM:193067		
CLASSIFICATION		#superfamily transcription factor erg; ets DNA-binding domain	
KEYWORDS		homology; ets RII regulatory region homology alternative splicing; DNA binding; nucleus; proto-oncogene; transcription factor; transforming protein	
FEATURE			
SUMMARY	6-84	#domain ets DNA-binding domain homology #label ETS	
		#length 173 #checksum 5090	
Query Match		Score 21.5%; Score 74%; DB 2; Length 173; Best Local Similarity 61.8%; Pred. No. 1.85e-124; Matches 110; Conservative 30; Mismatches 26; Indels 12; Gaps 11;	
Db	1	SGQIQLWQPLLESDSSNSCITWEGTINGEKFMDPDEVARNGEKRSPKPNMYDKLSR	60
QY	307	SGQIQLWQPLLESDSSNSCITWEGTINGEKFMDPDEVARNGEKRSPKPNMYDKLSR	366
Db	61	ALRYYDKNIMTKVHGKRYA-YKFDFAGLAQAMQPQVADPSMYRQ-SDTT-YLPGY-HP	116
ATURE	52-126	#map_P1:SGQIQLWQPLLESDSSNSCITWEGTINGEKFMDPDEVARNGEKRSPKPNMYDKLSR	
217-295	#length 385 #molecular-weight 43437 #checksum 4889		
SUMMARY			
Query Match	40-48:	Score 1401; DB 1; Length 385; Best Local Similarity 56.4%; Pred. No. 5.17e-265; Matches 229; Conservative 69; Mismatches 73; Indels 35; Gaps 21;	
RESULT	9	S51226 #type fragment	
ENTRY		transcription factor erg/fli-1 homolog - polychaete (Nereis diversicolor) (fragment)	
TITLE		# formal_name Nereis diversicolor # common_name sandworm	
ORGANISM		15-Jul-1995 #sequence_revision 23-May-1997 #text_change	
DATE		30-May-1997	
ACCESSIONS	S51226		
REFERENCE			
#authors		Leprince, D.; Fontaine, F.	
#journal		FBBS Lett. (1994) 354:62-66	
#title		Identification of two related genes in a marine worm, the polychaete annelid Nereis diversicolor.	
#accession		#note	
		preliminary	

CLASSIFICATION #residues 1-179 ##label LEI #superfamily transcription factor erg; ets DNA-binding domain homology; ets RII regulatory region homology
 KEYWORDS DNA binding; nucleus; transcription factor
 FEATURE SUMMARY #length 179 #checksum 4104

Query Match 19.9%; Score 631; DB 2; Length 179;
 Best Local Similarity 57.5%; Pred. No. 3 93e-113; Mismatches 104; Conservative 36; Mismatches 28; Indels 13; Gaps 12; Matches 7-85

Db 1 GSGQIQLWQFLELLSDSANSHITWEGTNGEFLKLYDPPDEARRGERKSPMNYDKLS 60
 Qy 306 GSGQIQLWQFLELLSDSSNSNCITWEGTNGEFLKMTDPDEARRGERKSPMNYDKLS 365

Db 61 RALRYYDKNMTKVHPESSNYKYP-SDLP-YMSSYHKGKRYAKFDFHGIAQLOPHAH 116
 Qy 366 RALRYYDKNMTKVHPESSNYKYP-SDLP-YMSSYHKGKRYAKFDFHGIAQLOPHAH 423

117 TSKNLNMMAHAP-MASSASGFPPPPARYWSSLVGSNLYPNTSNHAMSHHPOGHMSSHLGSY 175
 Qy 424 PQKMNVAHPHPALPVTSSEFAAPNPYWNSPGG-IYPN-T-R-LP--RAHMPHLGTY 477

Db 176 Y 176
 Qy 478 Y 478

RESULT 10
 ENTRY S28823 #type fragment
 TITLE transcription factor ets-21C - fruit fly (Drosophila melanogaster) (fragment)
 ALTERNATE_NAMES transforming protein ets-3
 ORGANISM transforming protein ets-6
 DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-May-1997

ACCESSIONS S28823
 REFERENCE S28823
 #authors Chen, T.; Bunting, M.; Karim, F. D.; Thummel, C. S.
 #journal Dev. Biol. (1992) 151:176-191
 #title Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain.

#accession S28823
 #molecule_type DNA
 #residues 1-103 ##label CHE
 #cross-references EMBL:M88475

GENETICS
 #gene Etts65A
 #cross-references FlyBase:FBgn0005658

CLASSIFICATION #superfamily transcription factor org; ets DNA-binding domain homology; ets RII regulatory region homology
 KEYWORDS DNA binding; nucleus; transcription factor

FEATURE #domain ets DNA-binding domain homology (fragment)
 #label ETS
 #length 94 #checksum 1156

SUMMARY

Query Match 13.5%; Score 467; DB 2; Length 94;
 Best Local Similarity 93.8%; Pred. No. 5 7.9e-67; Mismatches 4; Indels 0; Gaps 0; Matches 61; Conservative 93; Indels 0; Gaps 0;

Db 30 PGSGQIQLWQFLELLSDSNASCITWEGTNGEFLKLTDPDEARRGERKSPMNYDKL 89
 Qy 305 PGSGQIQLWQFLELLSDSSNSNCITWEGTNGEFLKMTDPDEARRGERKSPMNYDKL 364

Db 90 SRALR 94
 Qy 365 SRALR 369

RESULT 12
 ENTRY S11224 #type fragment
 TITLE transcription factor ets-1b - African clawed frog (fragment)
 ORGANISM formal_name Xenopus laevis #common_name African clawed frog
 DATE 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 08-Sep-1997

ACCESSIONS S11224
 REFERENCE S11224
 #authors Stiegler, P.; Wolff, C. M.; Baltzinger, M.; Hitzlitz, J.; Strehelin, D.; Bofort, N.; Reny, P.
 #journal Nuclic Acids Res. (1990) 18:5298
 #title Characterization of Xenopus laevis cDNA clones of the c-ots-1 proto-oncogene.

#cross-references MUID:90384849
 #accession S11224
 #molecule_type mRNA
 #residues 1-268 ##label STI

CLASSIFICATION #superfamily transcription factor ets; ets DNA-binding domain homology; ets RII regulatory region homology
 KEYWORDS DNA binding; nucleus; phosphoprotein; transcription factor

FEATURE #domain ets DNA-binding domain homology #label ETS
 #length 268 #checksum 3247

Query Match 13.2%; Score 458; DB 2; Length 268;
 Best Local Similarity 51.7%; Pred. No. 3 80e-65; Mismatches 60; Conservative 25; Mismatches 30; Indels 1; Gaps 1; Matches 8-96

Db 62 RALRYYDKNMTKVHPESSNYKYP-85
 Qy 366 RALRYYDKNMTKVHPESSNYK 390

RESULT 11
 ENTRY S28820 #type fragment

Query Match 13.2%; Score 458; DB 2; Length 268;
 Best Local Similarity 51.7%; Pred. No. 3 80e-65; Mismatches 60; Conservative 25; Mismatches 30; Indels 1; Gaps 1; Matches 8-96

Db 137 DRAELNKDKPVPAALAGYGSGIQLWQFLELLTDSSNSNCITWEGTNGEFLKMTD 196
 Qy 285 QRQDLPYQOLQPTSSRLANGSGQIQLWQFLELLTDSSNSNCITWEGTNGEFLKMTD 344

Matches 60; Conservative 25; Mismatches 30; Indels 1; Gaps 1;
Db 310 DRADINKDKPVIPAALAGTGSPIQLWQPLLELTDXSCOSIISWTGDGWERKLSDPD 369
Qy 285 QRPOLDPYQILGPPISSRLANGPSQIQLWQFLIELSDSSNSNCITWEGSINGEKFMTDPP 344
Db 370 EVARRWGERKSKPNNYDKLSRALRYYDKNIMKVHPPPESSMKVIPSQDLPYMSY 424
Qy 345 EVARRWGERKSKPNNYDKLSRALRYYDKNIMKVHPPPESSMKVIPSQDLPYMSY 400

Search completed: Wed Apr 7 09:44:31 1999
Job time : 78 secs.

FT	CHAIN	1	462	TRANSFORMING PROTEIN ERG-2.
FT	CHAIN	100	462	TRANSFORMING PROTEIN ERG-1.
DNA_BIND		294	374	ETS DOMAIN.
SEQUENCE	462 AA:	52031 MW;	CBCC2D2B CRC32;	
Query Match	Best Local Similarity	75.2%	Score 2608; DB 1; Length 462;	
Matches	396; Conservative	82.7%	Pred. No. 0.00e+00; Indels 27; Gaps 10;	
Best Local Similarity	82.7%; Pred.	82.7%;	Mismatches 29; Indels 27; Gaps 10;	
9	AHHIKEALSVVSDQSLFECAYGSPHLAKTEMATSSSSPYGOTSKMSPRVQDQLSQQP	68	68	
2	ASTIKEALSVVSDQSLFECAYGSPHLAKTEMATSSSSPYGOTSKMSPRVQDQLSQQP	61	61	
69	ARVTIKHECNPSQYNGSNSNPDCGSVAKGGKMGKSPDTGMYNGSYMEKKHMPPPNMNTN	128	128	
62	ARVTIKHECNPSQYNGSNSNPDCGSVAKGGKMGKSPDTGMYNGSYMEKKHMPPPNMNTN	121	121	
129	ERRVIVADPTLWSTDHQRQLEWAKEYGLPDVNILEQNIDGKELCKMKTDDFORLT	188	188	
122	ERRVIVADPTLWSTDHQRQLEWAKEYGLPDVNILEQNIDGKELCKMKTDDFORLT	181	181	
189	SYNADILSLSHLHYLRETDPLPHLTSDDVDKALQNSPRIMARNTD---I-P---Y-E--	236	236	
182	SYNADILSLSHLHYLRETDPLPHLTSDDVDKALQNSPRIMARNTGATIFPNTSVPEA	241	241	
237	-----P-P---RRSAWTGIGHTPOSKAAQSPSPSTWPKTDQRPQDPYQIGPSS	284	284	
242	QRTTRDPDLYFQARRSAWTSWSHPT-OSKATOPSSSTPKTEDORPQDLPYQIGPSS	300	300	
285	RLANPGSGQIQWMQFULELLSDSSNSNCITTWGTTNGEKFMTDDEVARRGERKSPPNN	344	344	
301	RLANPGSGQIQWMQFULELLSDSSNSNCITTWGTTNGEKFMTDDEVARRGERKSPPNN	360	360	
345	YDKLSRALRYYYDKNIMTKVHGKRYAVKFDHGIAQALQPHPPESLYKP-SDLPYMGSS	403	403	
361	YDKLSRALRYYYDKNIMTKVHGKRYAVKFDHGIAQALQ	419	419	
404	YHAPQKMNFWVPHPLPVISSFFEARPNPYNSPPIGGIYPPTRLPSPHMPHSILGTY	462	462	
420	PHAPQKMNFWVPHPLPVISSFFEARPNPYNSPPIGGIYPPTRLPSPHMPHSILGTY	478	478	
RESULT	2			
ID	HUMAN	STANDARD;	PRY;	452 AA.
AC	001543;			
DT	01-JUL-1993 (REL. 26, CREATED)			
DT	01-NOV-1993 (REL. 26, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
FLI1	ONCOGENE (ERBB TRANSCRIPTION FACTOR).			
FILI	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
[1]	SEQUENCE FROM N.A.			
RC	TISSUE-BONE MARROW;			
RX	MEDLINE: 92396239.			
RA	DELAUTURE O., ZUCMAN J., PLOUGASTEL B., DESMAZE C., MELOT T.,			
RA	PETER M., KOVAR H., JOUBERT I., DE JONG P., ROULEAU G.;			
RL	NATURE 359:162-165(1992).			
RN	[2]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE: 93075640.			
RA	WATSON D.K., SMITH F.E., THOMPSON D.M., CHENG J.Q., TESTA J.R.,			
RA	PAPAS T.S., SETH A., CELL GROWTH DIFFER. 3:705-713(1992).			
RN	[3]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE: 93075640.			
RA	PRasad D.D., RAO V.N., REDDY E.S., CANCER RES. 52:5833-5837(1992).			
RN	[4]			
SEQUENCE FROM N.A.				
RC	TISSUE=BLOOD;			
RX	MEDLINE: 93176799.			
RA	HRomas R., MAY W., DENNY C., RASKIND W., MOORE J., MAKI R.A., BECK E., KLEMZ W. J.; BIOCHIM. BIOPHYS. ACTA 1172:155-158(1993).			
RN	[5]			
STRUCTURE BY NMR OF 276-73.				
RX	MEDLINE: 9522091.			
RA	Liang H., Mao X., Olejniczak E.T., Nettsheim D.G., Yu L., MEADOWS R.P., Thompson C.B., Fesik S.W.; NAT. STRUCT. BIOL. 1:871-875(1994).			
RL	THE DNA SEQUENCE 5'C'CA[GAGCT-3'.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.			
CC	-1- DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(11;22)(Q24;Q12) WHICH INVOLVES FLI1 AND EWS.			
CC	-1- SIMILARITY: BELONGS TO THE ETS FAMILY.			
DR	EMBL: X67001; G3250;			
DR	EMBL: M98933; G18219;			
DR	EMBL: S45005; G25734;			
DR	EMBL: M9355; G18260;			
PDB	1FL1 15-SEP-95.			
TRANSPAC	T02006;			
DR	MIN: 19307;			
DR	PROSITE: PS00345; ETS_DOMAIN_1;			
DR	PROSITE: PS00346; ETS_DOMAIN_2;			
DR	PROSITE: PS50061; ETS DOMAIN 3;			
KW	TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN; PROTO-ONCOGENE; CHROMOSOMAL TRANSLOCATION; 3D-STRUCTURE.			
FT	DNA_BIND	281	361	ETS-DOMAIN
FT	CONFLICT	69	69	E->V (IN REF. 4).
FT	CONFLICT	77	77	MISSING (IN REF. 4).
FT	CONFLICT	130	130	P->A (IN REF. 4).
FT	CONFLICT	133	133	W->V (IN REF. 4).
FT	CONFLICT	323	323	Y->O (IN REF. 3 AND 4).
FT	CONFLICT	391	391	Y->O (IN REF. 2 AND 4).
FT	CONFLICT	425	426	MISSING (IN REF. 2 AND 4).
SQ	SEQUENCE	452 AA;	50982 MW;	192476F7 CRC32;
Query Match	Best Local Similarity	51.2%	Score 1776; DB 1; Length 452;	
Matches	278; Conservative	57.4%	Pred. No. 0.00e+00; Indels 86; Gaps 38; Mismatches 82;	
Best Local Similarity	57.4%; Pred.	57.4%;	Mismatches 82; Indels 38; Gaps 23;	
Db	1 MDGTTKEALSVVSDQSLFDSAYGAHPLKADMATGSDPDYQGDHKINPLPPQEWING	60	60	
Qy	1 MASTIKEALSVVSDQSLFECAYGSP-HLAKTEMATSSSSPYGOTSKMSPRVQDQLSQQP	59	59	
Db	61 P-VRYVKRKYD-HHNGSRESPVCVSISCSKLVGGGEENPMNTNSYMEKKHMPPPNMNTN	117	117	
Qy	60 PPARVTKMCNPQYNGSNSPDCGSVAKGGKMGKSPDTGMYNGSYMEKKHMPPPNMNTN	118	118	
Db	118 TTNERVIVADPTLWSTDHQRQLEWAKEYGLPDVNILEQNIDGKELCKMKTDDFORLT	177	177	
Qy	119 TTNERVIVADPTLWSTDHQRQLEWAKEYGLPDVNILEQNIDGKELCKMKTDDFORLT	178	178	
Db	178 ATTLVTEVLISHLHYLRETDPLPHLTSDDVDKALQNSPRIMARNTGATIFPNTSV	222	222	
Qy	179 LTPSNADILSLSHLHYLRETDPLPHLTSDDVDKALQNSPRIMARNTGATIFPNTSV	238	238	
Db	223 DSV-R--R-G-AWGNNMNG-LNKS-PPLG-GAQ---TISKVQEQRQDPDQIQLGP	269	269	
Qy	239 EATQRITRDPLPYFQARRSAWTSWSHPTOSKATOPSSSTPKTEDORPQDLPYQIGPSS	298	298	
Db	270 SSRANPGSGQIQWMQFULELLSDSSNSNCITTWGTTNGEKFMTDDEVARRGERKSPPN	329	329	
Qy	299 SSRANPGSGQIQWMQFULELLSDSSNSNCITTWGTTNGEKFMTDDEVARRGERKSPPN	358	358	
Db	330 NYDKLSRALRYYYDKNIMTKVHGKRYAVKFDHGIAQALQPHPTESMYKYP-SDISYM	388	388	
Qy	359 NYDKLSRALRYYYDKNIMTKVHGKRYAVKFDHGIAQALQPHPTESMYKYP-SDISYM	417	417	
Db	389 PSYHAKQKVNFVPHPPSPNVPVSSFFEGRASQWTSPGIGYVNPVNRHNPNTVPSHL	448	448	

QY	285	QRPOLDPYQILGPTSSRLANPGSGQIQWLQFELLELSDSSNSNCITWEGTNEEKWMDPD 344	RESULT 11	
DB	367	EVARRNGKRNKPKNMVEKLRSRGLRYYDKNIHTK-AGKRVVRFVCDLSILGY 421	ID ETS1- MOUSE STANDARD; PRT; 440 AA.	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DT	01-AUG-1992 (REL. 23, CREATED)	P22577; 061403;	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)	COMPANY, (1990),	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DE	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)	C-ETS-1 PROTEIN (P54).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
GN	ET51 OR ETS-1.	ET51 OR ETS-1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
OS	MUS MUSCULUS (MOUSE)	MUS MUSCULUS (MOUSE)	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
[1]	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RC	WATSON D.-K., SETH A., SMYTH F.-E., SCHWEINFEST C.-W., PAPAS T.-S.; IN, ONCOGENES, PAPAS T.-S., ED., PP. 221-232, GULF PUBLISHING COMPANY, HOUSTON, (1990).	WATSON D.-K., SETH A., SMYTH F.-E., SCHWEINFEST C.-W., PAPAS T.-S.; IN, ONCOGENES, PAPAS T.-S., ED., PP. 221-232, GULF PUBLISHING COMPANY, HOUSTON, (1990).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RL	GUNTHER C.-V., NYE J.-A., BRYNER R.-S., GRAVES B.-J.; GENES DEV. 4:667-679(1990).	GUNTHER C.-V., NYE J.-A., BRYNER R.-S., GRAVES B.-J.; GENES DEV. 4:667-679(1990).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RN	[31]	[31]	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RC	STRAIN-BALB/C; TISSUE=THYMUS;	STRAIN-BALB/C; TISSUE=THYMUS;	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RX	MEDLINE: 90299137.	MEDLINE: 90299137.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RA	RA GUNTHER J.-H.; GENES DEV. 4:667-679(1990).	RA GUNTHER C.-V., NYE J.-A., BRYNER R.-S., GRAVES B.-J.; GENES DEV. 4:667-679(1990).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RN	[4]	[4]	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RP	STRUCTURE BY NMR OF 332-415.	STRUCTURE BY NMR OF 332-415.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RX	MEDLINE: 96176767.	MEDLINE: 96176767.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RA	RA DONALDSON L.-W., PETERSEN J.-M., GRAVES B.-J., MCINTOSH L.-P.; EMBO J. 15:125-134(1996).	RA DONALDSON L.-W., PETERSEN J.-M., GRAVES B.-J., MCINTOSH L.-P.; EMBO J. 15:125-134(1996).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RL	CHEN J.-H.; ONCOGENE RES. 5:277-285(1990).	CHEN J.-H.; ONCOGENE RES. 5:277-285(1990).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
CC	-I SIMILARITY: BEGINS TO THE ETS FAMILY.	-I SIMILARITY: BEGINS TO THE ETS FAMILY.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
CC	-I SIMILARITY: BELONGS TO THE ETS FAMILY.	-I SIMILARITY: BELONGS TO THE ETS FAMILY.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	EMBL: M58462; G193192; -.	EMBL: M58462; G193192; -.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	EMBL: X53953; G30871; -.	EMBL: X53953; G30871; -.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	EMBL: X55787; G296023; -.	EMBL: X55787; G296023; -.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	A30487; A30487.	A30487; A30487.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	PDB: 1ETD; 29-JAN-96.	PDB: 1ETD; 29-JAN-96.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	TRANSTAC; T00111; -.	TRANSTAC; T00111; -.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
MGD	MGD: MGI:93455; ETS1.	MGD: MGI:93455; ETS1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
PROSITE	PROSITE; PS0045; ETS_DOMAIN_1; 1.	PROSITE; PS0045; ETS_DOMAIN_1; 1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
PROSITE	PROSITE; PS00346; ETS_DOMAIN_2; 1.	PROSITE; PS00346; ETS_DOMAIN_2; 1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
PROSITE	PROSITE; PS00061; ETS_DOMAIN_3; 1.	PROSITE; PS00061; ETS_DOMAIN_3; 1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
KW	PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; PHOSPHORYLATION; 3D-STRUCTURE.	PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; PHOSPHORYLATION; 3D-STRUCTURE.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	DNA-BIND 335 415 ETS-DOMAIN.	DNA-BIND 335 415 ETS-DOMAIN.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 28 28 D -> E (IN REF. 1 AND 3).	CONFICT 28 28 D -> E (IN REF. 1 AND 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 37 37 L -> S (IN REF. 3).	CONFICT 37 37 L -> S (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 51 52 AT -> SY (IN REF. 3).	CONFICT 51 52 AT -> SY (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 55 55 G -> P (IN REF. 1).	CONFICT 55 55 G -> P (IN REF. 1).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 63 63 L -> R (IN REF. 3).	CONFICT 63 63 L -> R (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 74 74 E -> D (IN REF. 3).	CONFICT 74 74 E -> D (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 96 96 Q -> H (IN REF. 3).	CONFICT 96 96 Q -> H (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 105 105 L -> V (IN REF. 3).	CONFICT 105 105 L -> V (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 157 157 D -> V (IN REF. 3).	CONFICT 157 157 D -> V (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 211 211 Q -> R (IN REF. 3).	CONFICT 211 211 Q -> R (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 217 217 D -> E (IN REF. 3).	CONFICT 217 217 D -> E (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 225 225 A -> R (IN REF. 3).	CONFICT 225 225 A -> R (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 234 234 D -> N (IN REF. 3).	CONFICT 234 234 D -> N (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 360 360 G -> C (IN REF. 3).	CONFICT 360 360 G -> C (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 383 383 K -> S (IN REF. 3).	CONFICT 383 383 K -> S (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	CONFICT 392 392 G -> A (IN REF. 3).	CONFICT 392 392 G -> A (IN REF. 3).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
QY	345 EVARRNGERKSKPNMNYDKLSRALYYDKNIMTKVHPPESSMYKPSDLPMYSSY 400	345 EVARRNGERKSKPNMNYDKLSRALYYDKNIMTKVHPPESSMYKPSDLPMYSSY 400	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DB	310 DRADLNKDKPVIPAAALLAGYTGGSPQIQWQFLELLTDKSCOSFISMGDGNEFKLSDPD 369	310 DRADLNKDKPVIPAAALLAGYTGGSPQIQWQFLELLTDKSCOSFISMGDGNEFKLSDPD 369	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DE	C-ETS-1 PROTEIN (P54).	C-ETS-1 PROTEIN (P54).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
GN	ET51 OR ETS-1.	ET51 OR ETS-1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
OS	RATTUS NORVEGICUS (RAT).	RATTUS NORVEGICUS (RAT).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RN	[1]	[1]	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RX	RA BELLAGOSA A., DATTA K., BEAR S.E., PATRIOTIS C., LAZO P.A., COPELAND N.G., JENKINS N.A., TSICHLIS P.N.; J. VIROL. 66:2320-2330(1992).	RA BELLAGOSA A., DATTA K., BEAR S.E., PATRIOTIS C., LAZO P.A., COPELAND N.G., JENKINS N.A., TSICHLIS P.N.; J. VIROL. 66:2320-2330(1992).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RA	RA COPELAND N.G., JENKINS N.A., TSICHLIS P.N.; J. VIROL. 66:2320-2330(1992).	RA COPELAND N.G., JENKINS N.A., TSICHLIS P.N.; J. VIROL. 66:2320-2330(1992).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RL	RL J. VIROL. 66:2320-2330(1992).	RL J. VIROL. 66:2320-2330(1992).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
CC	CC -I SIMILARITY: SUBCELLULAR LOCATION: NUCLEAR.	CC -I SIMILARITY: SUBCELLULAR LOCATION: NUCLEAR.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DR	DR PROSITE; PS00061; ETS_DOMAIN_3; 1.	DR PROSITE; PS00061; ETS_DOMAIN_3; 1.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
KW	KW PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; PHOSPHORYLATION; 3D-STRUCTURE.	KW PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; PHOSPHORYLATION; 3D-STRUCTURE.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
FT	FT DNA_BIND 335 415 ETS-DOMAIN.	FT DNA_BIND 335 415 ETS-DOMAIN.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
Db	310 DRADLNKDKPVIPAAALLAGYTGGSPQIQWQFLELLTDKSCOSFISMGDGNEFKLSDPD 369	310 DRADLNKDKPVIPAAALLAGYTGGSPQIQWQFLELLTDKSCOSFISMGDGNEFKLSDPD 369	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
QY	285 QRQLDPYQILGPTTSRLANPGSGQIQWLQFELLELSDSSNSNCITWEGTNEEKWMDPD 344	285 QRQLDPYQILGPTTSRLANPGSGQIQWLQFELLELSDSSNSNCITWEGTNEEKWMDPD 344	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
Db	370 EVARRNGERKSKPNMNYDKLSRALYYDKNIMTKVHPPESSMYKPSDLPMYSSY 424	370 EVARRNGERKSKPNMNYDKLSRALYYDKNIMTKVHPPESSMYKPSDLPMYSSY 424	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
QY	345 EVARRNGERKSKPNMNYDKLSRALYYDKNIMTKVHPPESSMYKPSDLPMYSSY 400	345 EVARRNGERKSKPNMNYDKLSRALYYDKNIMTKVHPPESSMYKPSDLPMYSSY 400	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
ID	ID ETS1_HUMAN STANDARD; PRT; 441 AA.	ID ETS1_HUMAN STANDARD; PRT; 441 AA.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
AC	AC P41156;	AC P41156;	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DT	DT 01-APR-1990 (REL. 14, CREATED)	DT 01-APR-1990 (REL. 14, CREATED)	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DT	DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)	DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
DE	DE C-ETS-1 PROTEIN (P54) (C-ETS-1A AND C-ETS-1B).	DE C-ETS-1 PROTEIN (P54) (C-ETS-1A AND C-ETS-1B).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
GN	GN ET51.	GN ET51.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
OS	OS HOMO SAPIENS (HUMAN).	OS HOMO SAPIENS (HUMAN).	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
OC	OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.	OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RN	RN [1]	RN [1]	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RP	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).
RX	RX 89083219.	RX 89083219.	AC P41156;	FT CONFLICT 408 409 413 KR -> NA (IN REF. 3). R -> A (IN REF. 3).

RA REDDY E.S.P., RAO V.N.; RX MEDLINE: 90356411.
 RL ONGENE RES. 3:239-246(1988). RA WOLFF C.M., STIEGLER P., BAUTZINGER M., MEYER D., GHYSDAEL J.,
 RN [2] RA STEHELIN D., BEFOR N., REMY P.;
 SEQUENCE FROM N.A. RL NUCLEIC ACIDS RES. 18:4503-4504(1990).
 MEDLINE; 89042086. RN [3]
 WATSON D.K., MCWILLIAMS M.J., LAPTS P., LAUTENBERGER J.A., RP SEQUENCE OF 121-472 FROM N.A.
 RA SCHWEINEST C.W., PAPAS T.S.; RX MEDLINE: 92058972.
 PROC. NATL. ACADE. SCI. U.S.A. 85:7862-7866(1988). RA WOLFF C.M., STIEGLER P., BAUTZINGER M., MEYER D., GHYSDAEL J.,
 RN [3] RA STEHELIN D., BEFOR N., REMY P.;
 STRUCTURE BY NMR OF 32D-415. RL CELL GROWTH DIFFER. 2:447-55(1991).
 MEDLINE; 96097120. CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 RA WERNER M.H., CLORE G.M., FISHER C.L., FISHER R.J., TRINH L., SHILOACH J., GRONBORN A.M.; CELL 83:751-771(1995).
 RA -1- SUBCELLULAR LOCATION: NUCLEAR.
 RL -1- PTM: ISOFORMS OF ETS-1 ARE ALSO GENERATED BY DIFFERENTIAL
 CC PHOSPHORYLATION. -1- DISEASE: ETS IS RESPONSIBLE FOR ERYTHROBLAST AND FIBROBLAST
 CC TRANSFORMATION. THE JUXTAPOSITION OF THE INTERFERON AND C-ETS-1 PROTO-ONGENE MAY BE INVOLVED IN THE PATHOGENESIS OF HUMAN MONOCYTIC LEUKEMIA.
 CC -1- ALTERNATIVE PRODUCTS: ISOFORMS OF ETS-1 CAN BE GENERATED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 DR EMBL: X14798; G29882; -; DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR EMBL: X14798; G29882; -; DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
 DR EMBL: X14798; G29882; -; DR DNA-BINDING; NUCLEAR PROTEIN.
 DR PIR: A32066; TYHUM. DR DNA_BIND 366; NUCLEAR ETS-DOMAIN.
 DR PIR; S10866; S10866. FT SQ 472 AA; 53894 MW; 064D44EA CRC32;
 DR PDB: 2STW; 12-MAR-97. Query Match 13 1%; Score 453; DB 1; Length 472;
 DR TRANSFAC; T00112; -. Best Local Similarity 59.2%; Pred. No. 3.6e-74; Matches 61; Conservative 24; Indels 2; Gaps 2;
 DR MM: 164720; -. DR 354 ASTIAGFTGSGPIQLWQFLLELLTDKSCQSFIWTGWDGWEEKFLTDPEVARRGKRNKP 413
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1. DR 299 SSRLAN-PGSGQIQLWQFLLELLTDKSCQSFIWTGWDGWEEKFLTDPEVARRGKRNKP 357
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1. DR 414 KMNYEKLSRGRLYYDRNIIKHT-SGKRYVYRFVCDLQSHLY 455
 DR PROSITE; PS50061; ETS_DOMAIN_3; 1. DR 358 NMNIDKLSSLRALRYYYDRNIMTKVHPPESSMKYKPSDLPLPYMSYY 400
 KW PROTO-ONGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; SQ
 KW PHOSPHORYLATION; 3D-STRUCTURE. DR RESULT 15
 KW DNA_BIND 335 13 2%; Score 456; DB 1; Length 472;
 KW FT ID ETS_A_CHICK STANDARD; PRT; 441 AA.
 KW VASPPLIC 244 330 Best Local Similarity 59.2%; Pred. No. 3.6e-74; Matches 60; Conservative 24; Indels 2; Gaps 2;
 KW SEQUENCE 441 AA; 50408 MW; 958AFAM4 CRC32; DR 01-JAN-1990 (REL. 13, CREATED)
 Db 310 DRADLNKDKPVIPAALAGTGTGGCPIQLWQFLLELLTDKSCQSFIWTGWDGWEEKFLSPD 369 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 Db 285 QRPQDPYQIQLGTTSSRANPQGGQIQWLQFLLELLTDKSCQSFIWTGWDGWEEKFLSPD 344 DE TRANSFORMING PROTEIN PS4/C-ETS-1.
 Db 370 EVARRWGKRNPKMYEKLRSGTRYYDKNTIKHT-AGKRYVYRFVCDLQSHLY 424 GN ETS-1;
 Qy 345 EVARRWGERKSKPMWYDKLSSLRALRYYYDRNIMTKVHPPESSMKYKPSDLPLPYMSYY 400 OS GALLUS GALLUS (CHICKEN).
 OC EUARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; OC GALLIFORMES.
 OC [1] RN SEQUENCE FROM N.A.
 RN RP TISSUE-SPLEEN;
 RN MEDLINE; 88289026.
 RN DUFERRUE-COQUILLAUD M., LEPRINCE D., FLORENS A., HENRY C., RA GHYSDAEL J., DEBUJE C., STEHELIN D.,
 RN ONCOGENE RES. 2:335-344(1988). RL
 RN [2] SEQUENCE FROM N.A.
 RN RP TISSUE-SPLEEN;
 RN MEDLINE; 88289029.
 RN CHEN J.-H.; RA
 RN ONCOGENE RES. 2:371-384(1988). RL
 RN SEQUENCE FROM N.A. MEDLINE; 8904531.
 RN RA WATSON D.K., MCWILLIAMS M.J., PAPAS T.S.; RX
 RN Virology 167:1-7(1988). RL
 RN -1- FUNCTION: THIS PROTEIN IS THE NORMAL CELLULAR PRODUCT OF CHICKEN ETS. IN THE EBV VIRUS, ETS IS RESPONSIBLE FOR ERYTHROBLAST TRANSFORMATION.
 CC CC -1- TISSUE SPECIFICITY: THYMUS.
 CC CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING MECHANISM WITHIN THE CC ETS-1 GENE GENERATES TWO PROTEINS HAVING DISTINCT N-TERMINAL EXTREMITY: P54 AND P68.
 RC CC TISSUE=OOCYTE;

CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
DR M22462; G21153; -.
EMBL; X13026; G63180; -.
DR EMBL; X13027; G63383; -.
DR PIR; A3185; TWCHTE.
DR PIR; S07625; S07625.
DR PIR; S29132; S29132.
DR TRANSFAC; T0114; -.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS0061; ETS_DOMAIN_3; 1.
KW PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPlicing.
FT DNA_BIND 335 415 ETS-DOMAIN.
FT CONFLICT 117 117 R -> A (IN REF. 3).
FT SEQUENCE 441 AA; 50326 MW; 734839B3 CRC32;

Query Match 13.0%; Score 452; DB 1; Length 441;
Best Local Similarity 50.9%; Pred. No. 6.19e-74;
Matches 59; Conservative 26; Mismatches 30; Indels 1; Gaps 1;
Matches 59; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

310 DRADDMNKDKEVIPAAALAGWTGSGPQLMWFQFLLELTIDKSCQSFITSWIGDGWEKLSDPD 369
:|::: :|::: :||| |||||||||:||| :||| | ||::|||
Qy 285 QRQLDPLYQILGPSSRRLANPGSGQIQLNQFLLELSDDSNNSNCITWEGINGERKMTDD 344

Db 370 EVARRKGKRKKPKANYEKLSRGARYYDNNIHT-AGKRYVRFVCDLQSLGY 424
:||||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 345 EVARRKGKRKKPKANYDKLSRALRYYDKNIMTKVHPPPESSMKIPSDLPLYMSY 400

Search completed: Wed Apr 7 09:46:02 1999
Job time : 72 secs.

197 ERGAFIENNTSYPEAATORITRDLFBEQARRSAWISHPQSOKATOPSSS TVPKT 255
ORGANISM #*(Lytechinus variegatus)* fragment
#formal_name *Lytechinus variegatus* #common_name variegated
urchin

Db 188 TEORQPQPPQYQIQLGPTSSLANPGSGOIQLWOFLELLSDSANASCITWEGTNGERKMTD 247
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
08-Sep-1997

Db 256 EDORPOLDYQOLGPTSSRLANPGSGOIQLWOFLELLSDSSNSNCITWEGTNGERKMTD 315
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ACCESSIONS A56646
REFERENCE #authors OI, S.; Chen, Z.Q.; Papas, T.S.; Lautenberger, J.A.
#journal DNA Seq. (1992) 3:127-130
#title The sea urchin erg homolog defines a highly conserved
erg-specific domain.

Qy 248 PDEVARRGWERKSCKPNMNDKLSLRALLYDKNIMTKVKGKRYAKFEDHGIAQALQPH 307
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 316 PDEVARRGWERKSCKPNMNDKLSLRALLYDKNIMTKVKGKRYAKFEDHGIAQALQPH 375
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 TESSMKYPSDISMPSYRAHQKVNFVPPHSPSMVTSSFFGASQWMS-TGGIYN 366
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 376 PESSMKYPSDISMPSYRAHQKVNFVPPHSPSMVTSSFFGASQWMS-TGGIYN 435
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 367 PNYPHRPHVPHVPSHLGSY 385
:|| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:
Qy 436 T---RLPAAHMPSHLGTY 451
:|| :||:||:||:||:||:||:||:||:||:||:||:||:

SULT 7
TRY A54617 #type fragment
LITTLE transcription factor erg - mouse (fragment)
ORGANISM #formal_name *Mus musculus* #common_name house mouse
DATE 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
30-Oct-1997
ACCESSIONS A54617
A54617
#authors Rivera, R.R.; Stuiver, M.H.; Steenbergen, R.; Murre, C.
#journal Mol. Cell. Biol. (1993) 13:7153-7169
FEATURE #title Ets proteins: new factors that regulate immunoglobulin
across-references MUD:94019387
#accession A54617
KEYWORDS #status preliminary
#molecule_type mRNA
#residues 1-272 #label RIV
#note #experimental_source pre-B-cell line 22D6
#sequence extracted from NCBI backbone (NCBIN:138523,
NCBIL:13824)

CLASSIFICATION #superfamily transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology
DNA binding; phosphoprotein; proto-oncogene; transcription
factor; transforming protein

FEATURE 140-218
#domain ets DNA-binding domain homology #label ETS
SUMMARY #length 272 #checksum 3754

RESULT 9
ENTRY S51226 #type fragment
TITLE transcription factor erg/fil-1 homolog - polychaete (*Nereis*

ORGANISMdiversicolor

DATE(fragment)

ACCESSIONSdiversicolor

REFERENCEdiversicolor

#authorsLeprince, D.; Fontaine, F.

#journalFEMS Lett. (1994) 334:62-66

#titleIdentification of two ets related genes in a marine worm, the
polychaete annelid *Nereis diversicolor*.

#accessionS51226

#statuspreliminary

#molecule_typeDNA

#residues1-179 #label IEL

CLASSIFICATION #superfamily transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology
DNA binding; nucleus; transcription factor

FEATURE 7-85
#domain ets DNA-binding domain homology #label ETS
SUMMARY #length 179 #checksum 4104

RESULT 8
ENTRY A55646 #type fragment
TITLE Transcription factor erg/fil-1 homolog - sea urchin

Db 1 GSGQIQLWOFLELLSDSSNSNCITWEGTNGERKLVDPDETARRGERSKPNMYDKLS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 279 GSQQIQLWOFLELLSDSSNSNCITWEGTNGERKLVDPDETARRGERSKPNMYDKLS 338
:|||||:|||||:|||||:|||||:

Db 61 RALRYYDKNMTKVKGKRYKDFGGLADQMQSPSTDPAKYQODL-LMSGYH-HTS 118
 Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 339 RALRYYDKNMTKVKGKRYKDFGGLADQMQSPSTDPAKYQODL-LMSGYH-HTS 118
 Db 119 KNLMLMAHAP-MASSASGEFPFPAPWSSLVGSNLYPNISHAMSHPGHMSHIGSYV 176
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 399 KWNFVAPRHPALPVTSFFAFNPVNPNVSPICG-TYPN-T-R-LP--AAHMPSHLGTY 451
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 RESULT 10 S37616 #type complete
 ENTRY transcription factor elg - fruit fly (drosophila
 TITLE melanogaster)
 ALTERNATE_NAMES transcription factor elg-97D
 ORGANISM formal name Drosophila melanogaster
 DATE 13-Sep-1995 #sequence_revision 23-May-1997 #text_change
 18-Sep-1998 S37616; S28822
 ACCESSIONS S37616
 REFERENCE The, S.M.; Xie, X.; Smyth, F.; Papas, T.S.; Watson, D.K.; Schulz, R.A.
 #authors Oncogene (1992) 7:2471-2478
 #journal Molecular characterization and structural organization of D-olig, an ets proto-oncogene-related gene of Drosophila.
 #accession S37616
 #status preliminary
 #molecule-type DNA
 #residues 1-464 #label THE
 #cross-references S28819; EMBL:68259; NID:97942; PID:97943
 REFERENCE Dev. Biol. (1992) 151:176-191
 Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S.
 Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain.
 #accession S28822
 #molecule-type mRNA
 #residues 298-449 #label CHE
 #cross-references EMBL:68471; NID:915189; PID:9552088
 #note the authors translated the codon AGC for residue 302 as Thr
 GENETICS
 #gene FlyBase:Ets97D
 #cross-references FlyBase:FBgn0004510
 CLASSIFICATION #superfamily transcription factor elg; ets DNA-binding domain homology; ets RII regulatory region homology
 KEYWORDS DNA binding; nucleus; transcription factor
 FEATURE 190-263
 #domain ets RII regulatory region homology #label ERR\\
 SUMMARY #domain ets DNA-binding domain homology #label ETS #length 464 #molecular-weight 52658 #checksum 2714
 Query Match 20.1%; Score 660; DB 1; Length 464;
 Best Local Similarity 39.6%; Pred. No. 2.17e-107;
 Matches 97; Conservative 62; Mismatches 74; Indels 12; Gaps 11;
 Db 192 EORLKPEAANEWTHAHVTWLEAVKQFELVGINNSDWQ-MNGQELCAMHEEFLKL 250
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 121 NERRVTPADPTLWSTDHVRQLEAVKKEYGLPDVDFLQNDKECLCKMKTDF-ORL 179
 Db 251 -PRDPGIFWTHQLKE--GKV-SVHKRKE-QDKPKRIMANSISTN-SGSLS 304
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 180 TPSYNADILSLHYLNERGATFEPNTSVPEATQRITTRDLPYQARSAWTSHP 239
 Db 305 LEQRIMRKSYQSV-KSSD-SVE-STTSSMNPNVTTGSGNNQVOLWQFLLELTACEH 361
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 240 TOSKATOPSSSVPKEDQRQDLPQILGTS-SRLANPGSGQIQWQFLLELLSDSN 298
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 362 TDVIEWGTEGEFKLTDPPDRVRLWGGKKNKAMNZEKLSRALRYYDGDMISKSQRF 421
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 299 SNCITWEGTNGEKMTDDEVARWGERKSQPNMNYDKLSRALYYDKNIMTKVKGKRY 358
 Db 422 AYKFD 426

RESULT 11 A40858 #type complete
 ENTRY GA-binding protein alpha chain - mouse
 TITLE GABP; nuclear respiratory factor-2 alpha chain;
 ALTERNATE_NAMES transcription factor E4TF1 60k chain
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 28-Feb-1992 #sequence_revision 23-May-1997 #text_change
 10-Jul-1998 A40858
 ACCESSIONS A40858
 REFERENCE LaMarco, K.; Thompson, C.C.; Byers, B.P.; Walton, E.M.; McKnight, S.L.
 #authors Science (1991) 253:789-792
 #journal Identification of ets and notch-related subunits in GA
 #title #cross-references MUID:91343912
 #accession A40858
 #molecule-type mRNA; protein
 #residues 1-454 #label LAM
 #cross-references GB:MA4515; NID:9193382; PID:9193383
 #note parts of this sequence were determined by protein sequencing
 GENETICS
 #gene Gabpa
 #map_position 16 47.0
 COMPLEX GA-binding protein is a heterotetramer of two alpha and two beta-type chains.
 FUNCTION a transcription factor that binds (via the alpha chain) to
 #description known to promote transcription of apolipoprotein A-II,
 #pathway cytochrome c oxidase chain IV, ATPase beta chain, and adenovirus E4 genes
 CLASSIFICATION #superfamily transcription factor elg; ets DNA-binding domain homology; ets RII regulatory region homology
 KEYWORDS DNA binding; nucleus; transcription factor
 FEATURE 174-245
 #domain ets RII regulatory region homology #label ERR\\
 SUMMARY 322-400 #domain ets DNA-binding domain homology #label ETS #length 454 #molecular-weight 51363 #checksum 1760
 Query Match 19.9%; Score 653; DB 1; Length 454;
 Best Local Similarity 41.6%; Pred. No. 6.37e-06;
 Matches 101; Conservative 61; Mismatches 61; Indels 20; Gaps 15;
 Db 176 EQERLGIPYDPIWRSTDQVLLHVVWVTKERFSMTDIDLT-NISGRELCSELNOEDFFORY 234
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 121 NERRVTPADPTLWSTDHVRQLEAVKKEYGLPDVDFLQNDKECLCKMKTDF-ORL 179
 Db 235 -PR--GIIWASLELR-K---YVLASQE--QQMNE-IVVI-DQP-VQIIPAS-VPPATP 281
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 180 TPSYNADILSLHYLNERGATFEPNTSVPEATQRITTRDLPYQARSAWTSHP 239
 Db 282 TTIKVNS-SVAKAQ-NSRISGEDRSR-GNRGN-NGQIQWQFQELTDKDAR 336
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 240 TOSKATOPSSSVPKEDQRQDLPQILGTS-SRLANPGSGQIQWQFLLELLSDSN 299
 Db 337 DCISWYGDEGEFKLQNPQELVQKGWSORKNPKPTMNTERLSRALRYYDGDMISKSQRF 396
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 300 NCITWEGTNGEKMTDDEVARWGERKSQPNMNYDKLSRALYYDKNIMTKVKGKRY 359
 Db 397 YIF 399
 Qy ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 RESULT 12 A48146 #type complete
 ENTRY GA-binding protein alpha chain - human
 TITLE

Job time : 68 secs.

Search completed: Wed Apr 7 09:33:14 1999

FT CHAIN 1 462 TRANSFORMING PROTEIN ERG-2.
 FT CHAIN 100 462
 FT DNA_BIND 294 374 ETS-DOMAIN.
 FT SEQUENCE 462 AA; 52031 MW; CEC2D2B CRC32;

Query Match 91.0%; Score 2991; DB 1;
 Best Local Similarity 89.4%; Pred. No. 0.0e+00;
 Matches 405; Conservative 26; Mismatches 18; Indels 4; Gaps 4;
 RQ STRUCTURE BY NMR OF 276-373.
 RX TISSUE=BLOOD;
 RA MEDLINE; 93176799.
 RA HROMAS R., MAY W., DENNY C., RASKIND W., MOORE J., MAKI R.A.,
 RA BECK E., KLEMZ M.J.;
 RL BIOCHIM. BIOPHYS. ACTA 1172:155-158(1993).
 RN [5]

Db 9 AAIKEALSVVSEDDQSLFECAYGTPHLAKTENTASSSDYQOTSKMSPRVQDWTLSQPP 68
 Qy 2 ASTIKEALSVVSEDDQSLFECAYGSPHLAKTENTASSSEYQOTSKMSPRVQDWTLSQPP 61

Db 69 ARVTIKMECNPSQVNGSRNSPDECYAKGGKMGNSPDVGKMYGSNEEKHMPPRQDWLSQPP 68
 Qy 62 ARVTIKMECNPSQVNGSRNSPDECYAKGGKMGNSPDVGKMYGSNEEKHMPPRQDWLSQPP 61

Db 129 ERVIVYPADPLWSTHVRQLEWAVKEYGIPDVNLFLQNDKGELCKMTKDDQRLLTP 188
 Db 122 ERVIVYPADPLWSTHVRQLEWAVKEYGLPDVNLFLQNDKGELCKMTKDDQRLLTP 181
 Db 189 SYNADILSHLHYLRBERG-ATFFPPTSVYFEATORIT-TR-PDPYQARRSANTSHH 238
 Qy 182 SYNADILSHLHYLRBERG-ATFFPPTSVYFEATORIT-TR-PDPYQARRSANTSHH 238

Db 249 PTQPSQKAQPSPTSTVKTEDORPQLPYQIQLGPTSSRLANPGSGQIOLWQFLLELLSDSS 308
 Qy 239 PT-OSKATOPSSSTVPKTEDORPQLPYQIQLGPTSSRLANPGSGQIOLWQFLLELLSDSS 297

Db 309 NSSCTIWEGTNGEKFMDPVARRGERGERKSPPNMVYDKLSRALRYYYDKNIMTKVHGKR 368
 Qy 298 NSNCITWEGTNGEKFMDPVARRGERGERKSPPNMVYDKLSRALRYYYDKNIMTKVHGKR 357

Db 369 YAKEDFPHGTAQALQPHPESSLYKIPSDLPMGSIHAPKOMNFVAPHPPALPVTSSE 428
 Qy 358 YAKEDFPHGTAQALQPHPESSLYKIPSDLPMGSIHAPKOMNFVAPHPPALPVTSSE 417

Db 429 FAAPNPYWNNSPTGTYPNTRLPTSHMPHSLGTY 462
 Qy 418 FAAPNPYWNNSPTGTYPNTRLPTSHMPHSLGTY 451

RESULT 2
 ID FLII-HUMAN STANDARD; PRT; 452 AA.

Match 306; Conservative 85; Mismatches 55; Indels 11; Gaps 8;

Db 1 MDGTEALSVVSDDOSLDSEASAYGARAHIFKADMATGGSPDPYGOHKINPLPPOQEWINQ 60
 Qy 1 MASTIKEALSVVSEDDQSLFECAYGSP-HLAKTENTASSSEYQOTSKMSPRVQDWTLSQ 59

Db 61 P-VRVNVKRD-RHNGSSESPVDYCSCVKSKLVGGGSSNPNNMNSYDEKNGPPRN 117
 Qy 60 PPARTIKMECNPSQVNGSRNSPDECYAKGGKMGNSPDVGKMYGSNEEKHM-IPPNM 118

Db 118 TNERVIVYPADPLWSTHVRQLEWAVKEYGIPDVNLFLQNDKGELCKMTKDDQRLL 177
 Qy 119 TNERRVIVYPADPLWSTHVRQLEWAVKEYGLPDVNLFLQNDKGELCKMTKDDQRLL 178

Db 178 ATTLYNTEVILSHISYLRE-SSLAY-NTTSHQSSRLSVKEDPSYSVSRGAQNMN 235
 Qy 179 LTPSYNADILSHLHYLRBERGATEIPNVSVYFEATORITRDPLYQARRSANTSHH 238

Db 236 SGLNKSPPPLGAQTSKNTBQROPDPYQIQLGPTSSRLANPGSGQIOLWQFLLELLSDSA 295
 Qy 239 PTQSKATOPSS-TVPKTEDORPQLPYQIQLGPTSSRLANPGSGQIOLWQFLLELLSDSS 297

Db 296 NASCTIWEGTNGEKFMDPVARRGERGERKSPPNMVYDKLSRALRYYYDKNIMTKVHGKR 355
 Qy 298 NSNCITWEGTNGEKFMDPVARRGERGERKSPPNMVYDKLSRALRYYYDKNIMTKVHGKR 357

Db 356 YAKEDFPHGTAQALQPHPESSLYKIPSDLPMGSIHAPKOMNFVAPHPPALPVTSSE 415
 Qy 358 YAKEDFPHGTAQALQPHPESSLYKIPSDLPMGSIHAPKOMNFVAPHPPALPVTSSE 417

Db 416 FGAASQYWISPTGGIYVPNPVNPRHNPNTVPHSHLGYY 452

QY	418	FAPNPWNSPTGGIYNT--RLPAAHMPSHLGTYY	451
Db	356	YAYKEDFHFIAQALQPHPTTSWKKYPSDTSYMPHYSYHAQKVNVFVPSHSSMPVTSSF	415
Qy	358	YAYKEDFHFIAQALQPHPTTSWKKYPSDTSYMPHYSYHAQKVNVFVPSHSSMPVTSSF	415
Db	416	FGAASQWTSPTAGIYPNPSVPRIHTHYPSHLGYY	452
Qy	418	FAPNPWNSPTGGIYNT--RLPAAHMPSHLGTYY	451
Db	356	YAYKEDFHFIAQALQPHPTTSWKKYPSDTSYMPHYSYHAQKVNVFVPSHSSMPVTSSF	415
Qy	358	YAYKEDFHFIAQALQPHPTTSWKKYPSDTSYMPHYSYHAQKVNVFVPSHSSMPVTSSF	415
Db	416	FGAASQWTSPTAGIYPNPSVPRIHTHYPSHLGYY	452
Qy	418	FAPNPWNSPTGGIYNT--RLPAAHMPSHLGTYY	451
RESULT	3		
ID	FLII-1	STANDARD;	PRT;
AC	P26323;		452 AA.
DT	01-MAY-1992 (REL. 22, CREATED)		
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)		
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)		
DE	RETRORVIRAL INTEGRATION SITE PROTEIN FLI-1.		
GN	FLII OR FLI-1.		
OS	MUS; MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C; TISSUE-SPLEEN;		
RX	MEDLINE: 91257578.		
RX	BEN-DAVID Y., GIDDENS E.B., LETWIN K., BERNSTEIN A.; GENES DEV. 5: 908-918(1991).		
CC	[2]		
RP	CHARACTERIZATION.		
RX	MEDLINE: 92275657.		
RA	ZHANG L., LEMARCHEANDEL V., ROMEO P.-H., BEN-DAVID Y., GREER P., BERNSTEIN A.; ONCOGENE 8:1621-1630(1993).		
CC	-1- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RECOGNIZES THE DNA SEQUENCE 5'-C[CA]GGAACT-3'.		
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN BOTH HEMATOPOIETIC AND NONHEMATOPOIETIC TISSUES.		
CC	-1- INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLONES WITH F-MULV INSERTIONS UP-STREAM OF THE FLI-1 LOCUS.		
CC	-1- DISEASE: INVOLVED IN ERYTHROLEUKEMIA INDUCTION BY FRIEND MURINE LEUKEMIA VIRUS (F-MULV).		
CC	-1- SIMILARITY: BELONGS TO THE ETS FAMILY.		
DR	EMBL: X59421; G50975; -.		
DR	PIR: S17403; S17403.		
DR	TRANSFAC: T01408; -.		
DR	MGI: 9554; FLII.		
DR	PROSITE: PS00345; ETS DOMAIN 1; 1.		
DR	PROSITE: PS00346; ETS DOMAIN 2; 1.		
DR	PROSITE: PS0061; ETS DOMAIN 3; 1.		
KW	TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN; PROTO-ONCOGENE; PROSITE; PS00345; ETS DOMAIN 1; 1.		
FT	DNA_BIND_281	361	
FT	DNA_BIND_452_AA	452 AA;	51002 MW; CBCCACDDA CRC32;
Query Match	Best Local Similarity	70.1%	Score 2305; DB 1; Length 453;
Matches	302;	Conservative	Score 2305; DB 1; Length 453;
Matches	302;	Conservative	Score 2305; DB 1; Length 453;
DB	1	MDGTIKEALSIVWSDDQSLSFDSAYGAAAHLPKADMATASCGSSPDYQCPHKINPLPQQEWINQ	60
Qy	1	MASTIKEALSIVWSDDQSLSFDSAYGAAAHLPKADMATASCGSSPDYQCPHKINPLPQQEWINQ	59
DB	61	P-MRNYNIKREYE-HMNGRSRESPVDCSYKCNKLIGGSEGNAMEY-TYMDKEKGPPPNM	116
Qy	1	PMRNYNIKREYE-HMNGRSRESPVDCSYKCNKLIGGSEGNAMEY-TYMDKEKGPPPNM	116
DB	60	PPARTIKMCPNPQYNGNSNSPDCSVARGKMMSSDVNGWMNGSYMEKH-IPPPNM	118
DB	117	TNEERRVIVPADPAWLSQDHVRQWIEWAKEYLVEIDSLSFQNLTGKELCKMSIFDFLR	176
Qy	119	TNEERRVIVPADPAWLSQDHVRQWIEWAKEYLVEIDSLSFQNLTGKELCKMSIFDFLR	176
DB	177	STSTINTEVILSHLMLYLRLOSSSSGIGY-NIQTAHQDQSSRLTAKEDPSYEAUTRGNGNSMS	235
Qy	179	STSTINTEVILSHLMLYLRLOSSSSGIGY-NIQTAHQDQSSRLTAKEDPSYEAUTRGNGNSMS	235
DB	236	SPVTKSPPMGCTQVNKGQDQRSPDPQIQLGPSSRLANGPGSQIQLQWQFLLSDS	295
Qy	238	HPTSKATQPSSTSPTKPT-EDOPDQFDLPTQIQLGPSSRLANGPGSQIQLQWQFLLSDS	296
DB	296	SNASCTIWEGTNGETKMTDDEVAWRWGERKSKPKNNYDKLSRALRTRYYDKSIMVKHGK	355
Qy	297	SNSCTIWEGTNGETKMTDDEVAWRWGERKSKPKNNYDKLSRALRTRYYDKSIMVKHGK	356
DB	356	RYAYKEDFHFIAQALQPHPTTSWKKYPSDTSYMPHYSYHAQKVNVFVPSHSSMPVTSSF	415
Qy	357	RYAYKEDFHFIAQALQPHPTTSWKKYPSDTSYMPHYSYHAQKVNVFVPSHSSMPVTSSF	416

QY	318	EVARRGERKSKPMMYDKLSRALRYYDKNIMTKVHGKRYAKF	362
RESULT	13		
ID	ETSL_MOUSE	STANDARD;	PRT; 440 AA.
ID	AC	P27577; Q61403;	Score 14.9%; Score 490; DB 1; Length 440; Best Local Similarity 55.0%; Pred. No. 2.33e-83; Prid. 20; Mismatches 23; Indels 0; Gaps 0;
DT	01-AUG-1992 (REL. 23, CREATED)		
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
DE	C-ETS-1 PROTEIN (P54).		
GN	ETSL OR ETS-1.		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	WATSON D.K., SETH A., SMYTH F.E., SCHWEINFEST C.W., PAPAS T.S., (IN) ONCOGENESIS, PAPAS T.S., ED., PP. 221-232, GULF PUBLISHING COMPANY, HOUSTON, (1990).		
RL	[2]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/C; TISSUE=THYMUS;		
RX	MEDLINE; 9029913.		
RA	GUNTHER C.V., NYE J.A., BRYNER R.S., GRAVES B.J.; GENES DEV. 4:667-679(1990).		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RP	STRUCTURE BY NMR OF 332-415.		
RX	MEDLINE; 9617657.		
RA	DONALDSON L.W., PETERSEN J.M., GRAVES B.J., MCINTOSH L.P.; CHEN J.H.; ONCOGENE RES. 5:277-285(1990).		
RL	-1 - SUBCELLULAR LOCATION: NUCLEAR.		
CC	-1 - SIMILARITY: BELONGS TO THE ETS FAMILY.		
DR	EMBL: M58492; GI:913192; -.		
DR	EMBL: X53951; GS:0761; -.		
DR	EMBL: X55787; GS:29623; -.		
DR	PIR: A30487; A30487.		
DR	PDB: 1ETC; 29-JAN-96.		
DR	PDB: 1ETD; 29-JAN-96.		
DR	TRANSFAC; T0011; -.		
DR	MGD; MGI: 95455; ETS1.		
DR	PROSITE; PS00345; ETS_DOMAIN_1; 1.		
DR	PROSITE; PS00346; ETS_DOMAIN_2; 1.		
DR	PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; PHOSPHORYLATION; 3D-STRUCTURE.		
KW	DNA-BINDING		
FT	335 415		
FT	CONFFLICT 28 28		
FT	CONFFLICT 37 37		
FT	CONFFLICT 51 52		
FT	CONFFLICT 55 55		
FT	CONFFLICT 63 63		
FT	CONFFLICT 74 74		
FT	CONFFLICT 96 96		
FT	CONFFLICT 105 105		
FT	CONFFLICT 157 157		
FT	CONFFLICT 211 211		
FT	CONFFLICT 217 217		
FT	CONFFLICT 225 225		
FT	CONFFLICT 234 234		
FT	CONFFLICT 360 360		
FT	CONFFLICT 383 383		
FT	CONFFLICT 392 392		
FT	CONFFLICT 408 409		
FT	CONFFLICT 413 413		
FT	SEQUENCE 440 AA; 50201 MW; 18E90f01 CRC32;		
RESULT	14		
ID	ETSL_HUMAN	STANDARD;	PRT; 441 AA.
ID	AC	P14921;	
DT	01-APR-1990 (REL. 14, CREATED)		
DT	01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
DE	C-ETS-1 PROTEIN (P54) (C-ETS-1A AND C-ETS-1B).		
DN	ETSL.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 8908219.		
RA	REDDY E.S.P., RAO V.N.; SCHWEINFEST C.W., PAPAS T.S.;		
RL	ONCOGENE RES. 3:239-246(1988).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 89042086.		
RA	WATSON D.K., MCWILLIAMS M.J., LAPITS P., LAUTENBERGER J.A., SHILOACH J., GRONEMBORN A.M.;		
RL	PROC. NATL. ACAD. SCI. U.S.A. 85:7862-7866(1988).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 95097120.		
RA	WERNER M.H., CLORE G.M., FISHER C.L., FISHER R.J., TRINH L., SCHWEINFEST C.W., PAPAS T.S.;		
RL	CELL 83:761-771(1995).		
CC	-1 - SUBCELLULAR LOCATION: NUCLEAR.		
CC	-1 - PTM: ISOFORMS OF ETS-1 ARE ALSO GENERATED BY DIFFERENTIAL PHOSPHORYLATION.		
CC	-1 - DISEASE: ETS IS RESPONSIBLE FOR ERTHROBLAST AND FIBROBLAST TRANSFORMATION. THE JUXTAPOSITION OF THE INTERFERON AND C-ETS-1 PROTO-ONCOGENE MAY BE INVOLVED IN THE PATHOGENESIS OF HUMAN MONOCYTIC LEUKEMIA.		
CC	-1 - ALTERNATIVE PRODUCTS: ISOFORMS OF ETS-1 CAN BE GENERATED BY ALTERNATIVE SPLICING.		
CC	-1 - SIMILARITY: BELONGS TO THE ETS FAMILY.		
DR	EMBL: X14798; G29882; -.		
DR	EMBL: X14799; G29884; -.		
DR	EMBL: JO4101; G182269; -.		
DR	PIR: A330066; TVHUEH.		
DR	PIR: S10086; S10086.		
DR	PDB: 2STW; 12-MAR-97.		
DR	TRANSFAC; T00112; -.		
DR	MIM: 164720; -.		
DR	PROSITE; PS00345; ETS DOMAIN 1; 1.		
DR	PROSITE; PS00346; ETS DOMAIN 2; 1.		
DR	PROSITE; PS50061; ETS DOMAIN 3; 1.		
KW	PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING; PHOSPHORYLATION; 3D-STRUCTURE.		
FT	DNA-BIND 335 415		
FT	VARSPLIC 244 330		
SQ	SEQUENCE 441 AA; 50408 MW; 958AFA44 CRC32;		
Query Match	14.9%	Score 490; DB 1; Length 441;	
Best Local Similarity	59.0%	Pred. No. 2.33e-83; Pred. 20; Mismatches 23; Indels 0; Gaps 0;	
Matches	62;	Conservative; Mismatches 23; Indels 0; Gaps 0;	

Db 310 DRAIDLKKPKVTPAAALAGTGSGPQLQWFLLELITDKCQSFISWTGQGWEEKLSDPD 369
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 258 QRQLQDQYQTIGTGTSSRLAMPSSQIQOLWQFLLELLSDSSNSNCITWEGINGEFKMTDPD 317
 Db 370 EVARRNGKRKKPKPMYEKLSQLRGLRYYDKNTIKHAGKRYVRF 414
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 318 EVARRNGERKSPPNNYDQLSRALRVYYDKNIMTKVHGKRYAKF 362

RESULT 15
 ID ETS1-RAT STANDARD PRT; 441 AA.
 AC P41156;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE C-ETS-1 PROTEIN (P54).
 GN ETS1 OR ETS-1.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RP [1]
 SEQUENCE FROM N.A.
 RX MEDLINE; 94187072.
 RA BELLACOSA A., DATTA K., BEAR S.E., PATRIOTIS C., LAZO P.A.,
 RA COPELAND N.G., JENKINS N.A., TSICHLIS P.N.;
 RL J. VIROL. 68:2220-2230(1994);
 CC -I- SUBCELLULAR LOCATION: NUCLEAR.
 CC -I- SIMILARITY: BELONGS TO THE ETS FAMILY.
 DR EMBL; U20681; G404782; -.
 DR PIR; A53988; A53988.
 DR PROSITE; PS00345; ETS DOMAIN-1; 1.
 DR PROSITE; PS00346; ETS DOMAIN-2; 1.
 DR PROSITE; PS50061; ETS DOMAIN-3; 1.
 KW PROTO-ONCOENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING;
 KW PHOSPHORYLATION.
 FT DNA_BIND 335 415 ETS-DOMAIN.
 SQ SEQUENCE 441 AA; 50423 MW; 1C04335A CRC32;
 Query Match 14.9%; Score 490; DB 1; Length 441;
 Best Local Similarity 59.0%; Prod. No. 2.33e-83;
 Matches 62; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

Db 310 DRAIDLKKPKVTPAAALAGTGSGPQLQWFLLELITDKCQSFISWTGQGWEEKLSDPD 369
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 258 QRQLQDQYQTIGTGTSSRLAMPSSQIQOLWQFLLELLSDSSNSNCITWEGINGEFKMTDPD 317
 Db 370 EVARRNGKRKKPKPMYEKLSQLRGLRYYDKNTIKHAGKRYVRF 414
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 318 EVARRNGERKSPPNNYDQLSRALRVYYDKNIMTKVHGKRYAKF 362

Search completed: wed Apr 7 09:34:17 1999
 Job time : 47 secs.